

This Page Is Inserted by IFW Operations
and is not a part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

**As rescanning documents *will not* correct images,
please do not report the images to the
Image Problem Mailbox.**

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 23, 2003, 16:50:56 : Search time 24.5 Seconds

(Without alignments)
490.657 Million cell updates/sec

Title: US-09-865-321a-4_COPY_26_150
Perfect score: 657

Sequence: 1 AMHVAPAVYLASSRGIAF.....GIGNGTQIYVIDPEPCDDSD 125

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: PIR:*
2: PIR:*
3: PIR:*
4: PIR:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	634	96.5	223	2	cytotoxic T-lympho
2	631	96.0	186	2	cytotoxic T-lympho
3	552	84.0	223	2	cytotoxic T-lympho
4	453	68.9	223	2	cytotoxic T-lympho
5	150	22.8	221	2	CD28 protein - ch
6	137	20.9	173	2	cell surface prote
7	131	19.9	221	2	CD28 precursor - T
8	130.5	19.9	220	1	T-cell surface gly
9	121	18.4	218	2	T-cell surface gly
10	114	17.4	218	2	T-cell surface gly
11	94.5	14.4	140	2	ig kappa chain pre
12	93	14.2	124	2	ig kappa chain V-J
13	92.5	14.1	120	2	ig kappa chain V-J
14	90	13.7	125	2	ig kappa chain V-J
15	89.5	13.6	105	2	ig kappa chain V r
16	89.5	13.6	105	2	ig kappa chain V r
17	88.5	13.5	132	2	ig kappa chain V r
18	87.5	13.3	128	2	ig heavy chain V r
19	87	13.2	104	2	ig light chain var
20	87	13.2	108	2	anti-D-dimer monoc
21	86.5	13.2	108	2	ig kappa chain V r
22	86	13.1	111	1	ig kappa chain V r
23	85.5	13.0	212	2	ig lambda chain -
24	85	12.9	120	2	ig lambda chain V
25	85	12.9	129	2	ig kappa chain V
26	84.5	12.9	111	2	ig kappa chain - h
27	84.5	12.9	117	2	ig kappa chain V r
28	84.5	12.9	132	2	ig kappa chain V-J
29	84.5	12.9	213	2	ig kappa chain - h
					ig light chain pre

30	84	12.8	112	2	PL0274	ig kappa chain V r
31	83.5	12.7	106	2	PL0082	ig kappa chain V r
32	83.5	12.7	107	2	S12954	ig kappa chain V r
33	83.5	12.7	112	2	H26317	ig kappa chain V r
34	83	12.6	107	2	S36275	ig lambda chain V r
35	83	12.6	113	2	S30523	ig kappa chain V r
36	83	12.6	113	2	S34003	ig kappa chain V r
37	82.5	12.6	235	2	S14675	ig lambda chain -
38	82	12.5	108	2	G30560	ig kappa chain V r
39	82	12.5	133	2	S40378	ig kappa chain V r
40	81.5	12.4	79	2	A28840	ig kappa chain - h
41	81.5	12.4	130	2	A32513	ig kappa chain pre
42	81.5	12.4	197	2	S29593	ig kappa chain (NM
43	81.5	12.4	233	2	S29577	ig kappa chain - r
44	81.5	12.4	234	2	S14237	ig kappa chain pre
45	81	12.3	94	2	S26340	ig light chain V r

ALIGNMENTS

```

RESULT 1
T09536
cytotoxic T-lymphocyte protein 4 - human
C:Species: Homo sapiens (man)
C>Date: 16-Jul-1999 #sequence-revision 16-Jul-1999 #text-change 21-Jul-2000
C:Accession: T09536
R:Harper, K.; Balzano, C.; Rouvler, E.; Mattei, M.G.; Luciani, M.F.; Golstein, P.
J. Immunol. 147, 1037-1044, 1991
A:Title: CTLA-4 and CD28 activated lymphocyte molecules are closely related in both m
A:Reference number: I49584; MUID:91318145; PMID:1713603
A:Accession: T09536
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-223 <HAR>
A:Cross-references: EMBL:LI5006; NID:g291928; PIDN:AB59385.1; PID:g291929
A:Gene: CTLA4
A:Map position: 2q33
C:Superfamily: T-cell surface glycoprotein CD28; immunoglobulin homology
C:Keywords: T-cell; transmembrane protein

Query Match          96.5%  Score 634; DB 2; Length 223;
Best Local Similarity 97.6%  Pred. No. 1.9e-56;
Matches 122; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 AMHVAPAVYLASSRGIAFVCEYASPGKTEYRVYLRQADSQVEVCAATYMGNELT 60
        |||||
DB      37 AMHVAPAVYLASSRGIAFVCEYASPGKTEYRVYLRQADSQVEVCAATYMGNELT 96
        |||||

QY      61 FLDDICTGTSSGNQVNLITGIRAMDGLTYCKVELMPPPYEGTGTQIYVIDPEP 120
        |||||
DB      97 FLDDICTGTSSGNQVNLITGIRAMDGLTYCKVELMPPPYEGTGTQIYVIDPEP 156
        |||||

QY      121 CPDSD 125
        |||||
DB      157 CPDSD 161
        |||||

RESULT 2
S08614
cytotoxic T-lymphocyte protein 4 - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 07-Sep-1990 #sequence-revision 07-Sep-1990 #text-change 11-Jan-2000
C:Accession: S08614
R:Darlavach, P.; Mattei, M.G.; Golstein, P.; Iefranc, M.P.
Eur. J. Immunol. 18, 1901-1905, 1988
A:Title: Human ig superfamily CTLA-4 gene: chromosomal localization and identity of p
A:Reference number: S08614; MUID:89120925; PMID:3220103
A:Accession: S08614
A:Molecule type: DNA
A:Residues: 1-186 <DAR>
A:Cross-references: EMBL:X15070; NID:g30283; PID:g825649

```

C:Genetics:
 A:Gene: GDB:CTLA4
 A:Cross-references: GDB:119818; OMIM:123890
 A:Map position: 2q33-2q33
 A:Introns: 116/1; 152/3
 C:Superfamily: T-cell surface glycoprotein CD28; immunoglobulin homology
 C:Keywords: transmembrane protein
 F:123-150/Domain: transmembrane #status predicted <TM>
 F:151-186/Domain: intracellular #status predicted <INT>
 F:21-92/Disulfide bonds: #status predicted

Query Match
 Best Local Similarity 97.6%; Score 631; DB 2; Length 186;
 Matches 121; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 MHVAPAVYVLASSRGIAFVCEYASPGKYTEVRVTVLRQADSVTEVCATYMGNELTF 61
 DB 1 MHVAPAVYVLASSRGIAFVCEYASPGKATEVRVTVLRQADSVTEVCATYMGNELTF 60
 QY 62 LDDSTCTGTSSGNQVNLITQGLRAMDTGLYICKVELMPPPYEGISGNGTQIYVIDPEPC 121
 DB 61 LDDSTCTGTSSGNQVNLITQGLRAMDTGLYICKVELMPPPYLLGIGNAQIYVIDPEPC 120
 QY 122 PDSD 125
 DB 121 PDSD 124

RESULT 3

CTLA-4 precursor - rabbit
 A:Accession: I46696
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 05-Nov-1999
 A:Accession: I46696
 R:Isono, T.; Seto, A.
 Immunogenetics 42, 217-220, 1995
 A:Title: Cloning and sequencing of the rabbit gene encoding T-cell costimulatory molecule
 A:Reference number: I46689; MUID:95369849; PMID:7642234
 A:Accession: I46696
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-223 <ISO>
 A:Cross-references: GB:D49844; NID:9755100; PIDN:BA08644.1; PID:9755101
 C:Superfamily: T-cell surface glycoprotein CD28; immunoglobulin homology

Query Match
 Best Local Similarity 84.0%; Score 552; DB 2; Length 223;
 Matches 104; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 1 AMHVAOPAVYVLASSRGIAFVCEYASPGKYTEVRVTVLRQADSVTEVCATYMGNELTF 60
 DB 37 ALHVSQPAVYVLASSRGVASFCEYASPKATEVRVTVLRQANSQMTVEVCMTYVERELT 96
 QY 61 FLDDSTCTGTSSGNQVNLITQGLRAMDTGLYICKVELMPPPYEGISGNGTQIYVIDPEP 120
 DB 97 FIDDSCTGTGSHGNKVMITQGLSAMDTGLYICKVELMPPPYVGMGNGTQIYIEPEP 156
 QY 121 CPDSD 125
 DB 157 CPDSD 161

RESULT 4

A29063
 cytotoxic T-lymphocyte protein 4 - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 05-Nov-1999
 C:Accession: A29063; I49622
 R:Bruneet, J.F.; Dentzot, F.; Luciani, M.F.; Roux-Dosseto, M.; Suzan, M.; Mattei, M.G.; Nature 328, 267-270, 1987
 A:Title: A new member of the immunoglobulin superfamily--CTLA-4.
 A:Reference number: A29063; MUID:87258259; PMID:3496540
 A:Accession: A29063

A:Molecule type: mRNA
 A:Residues: 1-223

 A:Cross-references: GB:X05719; NID:950592; PIDN:CAA29191.1; PID:950593
 R:Harper, K.; Balzano, C.; Rouvier, E.; Mattei, M.G.; Luciani, M.F.; Golstein, P.
 J. Immunol. 147, 1037-1044, 1991
 A:Title: CTLA-4 and CD28 activated lymphocyte molecules are closely related in both m
 A:Reference number: I49584; MUID:91318145; PMID:1713603
 A:Accession: I49622
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-36 <RES>
 A:Cross-references: GB:M74362; NID:9192833; PIDN:AAA37489.1; PID:9553903
 C:Genetics:
 A:Gene: Ctla-4
 A:Map position: 1, band C
 C:Superfamily: T-cell surface glycoprotein CD28; immunoglobulin homology
 C:Keywords: transmembrane protein

Query Match
 Best Local Similarity 68.9%; Score 453; DB 2; Length 223;
 Matches 85; Conservative 16; Mismatches 24; Indels 0; Gaps 0;

QY 1 AMHVAOPAVYVLASSRGIAFVCEYASPGKYTEVRVTVLRQADSVTEVCATYMGNELTF 60
 DB 37 AIOVQPSVYVLASSRGVASFCEYSPSHNTDEVTVLRQNDQMTVEVCATFTTEKNTVG 96
 QY 61 FLDDSTCTGTSSGNQVNLITQGLRAMDTGLYICKVELMPPPYEGISGNGTQIYVIDPEP 120
 DB 97 FLDYPCSGTFNESHNRNLITQGLRAMDTGLYICKVELMPPPYFVGMGNGTQIYVIDPEP 156
 QY 121 CPDSD 125
 DB 157 CPDSD 161

RESULT 5

S25168
 CH728 protein - chicken
 C:Species: Gallus gallus (chicken)
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
 C:Accession: I50619; S25168
 R:Young, J.R.; Davison, T.F.; Tregaskes, C.A.; Rennie, M.C.; Vainio, O.
 J. Immunol. 152, 3848-3851, 1994
 A:Title: Monomeric homologue of mammalian CD28 is expressed on chicken T cells.
 A:Reference number: I50619; MUID:94194147; PMID:8144954
 A:Accession: I50619
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-221 <Y02>
 A:Cross-references: EMBL:X67915; NID:963221; PIDN:CAA48114.1; PID:963222
 C:Superfamily: T-cell surface glycoprotein CD28; immunoglobulin homology
 C:Keywords: transmembrane protein

Query Match
 Best Local Similarity 22.8%; Score 150; DB 2; Length 221;
 Matches 40; Conservative 21; Mismatches 45; Indels 12; Gaps 5;

QY 4 VAOPAVYVLASSRGIAFVCEYASPGKYTEVRVTVLRQADSVTEVCATYMGNELTFD 63
 DB 23 VAORPILIVANR-TATLVNCTYTYNGTKERFASLHGTDASV-EVCFISNM---TKIN 76
 QY 64 DSI-----CTGTSSGNQVNLITQGLRAMDTGLYICKVELMPPPY-YESGNGTQIYV 115
 DB 77 SNSNKEFNCRGHDKKVIENLMMSASQTDYFKIEAMYPYPPYVYNEKSNCTIVH 134

RESULT 6

I46197
 cell surface protein - dog (fragment)
 C:Species: Canis lupus familiaris (dog)
 C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
 C:Accession: I46197
 R:Pastori, R.L.; Milde, K.F.; Alejandro, R.

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 23, 2003, 16:43:01 ; Search time 13.5 Seconds

(without alignments)
435,432 Million cell updates/sec

Title: US-09-865-321a-4_COPY_26_150
Perfect score: 657
Sequence: 1 AMHVAQPAVVLASSRGIASF.....GICNGTQIYIDPEPCDSD 125

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	640	97.4	223	1	CTL4_HUMAN
2	552	84.0	223	1	PA2072 oryctolagus
3	549	83.6	223	1	CTL4_PIG
4	453	68.9	223	1	CTL4_MOUSE
5	150	22.8	221	1	CD28_CHICK
6	133.5	20.3	219	1	CD28_BOVIN
7	131	19.9	221	1	CD28_HUMAN
8	130.5	19.9	220	1	CD28_HUMAN
9	121	18.4	218	1	CD28_MOUSE
10	114	17.4	218	1	CD28_MOUSE
11	86	13.1	111	1	KV12_RABIT
12	81	12.3	129	1	HV2F_HUMAN
13	80.5	12.3	108	1	KV1G_HUMAN
14	80	12.2	739	1	VCA1_RAT
15	79.5	12.1	111	1	LV2E_HUMAN
16	79	12.0	111	1	LV2D_HUMAN
17	79	12.0	480	1	SAHH_XANCP
18	78	11.9	688	1	STLB_HUMAN
19	77.5	11.8	108	1	KV08_RABIT
20	77.5	11.8	108	1	KV1H_HUMAN
21	77.5	11.8	113	1	KV2G_MOUSE
22	77	11.7	111	1	LV2A_HUMAN
23	76.5	11.6	108	1	KV6K_MOUSE
24	76.5	11.6	149	1	KV5A_MOUSE
25	76	11.6	109	1	KV3E_HUMAN
26	76	11.6	109	1	KV4A_HUMAN
27	75.5	11.5	108	1	KV07_RABIT
28	75.5	11.5	113	1	KV2C_MOUSE
29	75.5	11.5	3707	1	PGBM_MOUSE
30	75	11.4	366	1	CD14_MOUSE
31	75	11.4	1356	1	VGR2_HUMAN
32	74.5	11.3	109	1	KV01_RAT
33	74.5	11.3	109	1	LV2E_HUMAN

34	74.5	11.3	113	1	KV2F_MOUSE	P01630 mus musculus
35	74.5	11.3	436	1	HSLU_RHILIO	O96cul rhizobium 1
36	74	11.3	480	1	SAHH_XYIFR	O9pej1 xyfella fas
37	74	11.3	715	1	LCCL_LACIA	O9cjb8 lactococcus
38	73.5	11.2	111	1	LV2C_HUMAN	P20956 xenopus lae
39	73.5	11.2	136	1	HY01_XENLA	P01634 mus musculus
40	73.5	11.2	136	1	KV5B_MOUSE	O9ye49 bruceella me
41	73.5	11.2	466	1	SAHH_BRONE	P01716 homo sapien
42	73	11.1	106	1	LV4B_HUMAN	P01629 mus musculus
43	73	11.1	112	1	KV2D_MOUSE	P01722 homo sapien
44	73	11.1	112	1	LV6B_HUMAN	P01774 homo sapien
45	73	11.1	119	1	HV3M_HUMAN	

ALIGNMENTS

RESULT 1
ID CTL4_HUMAN STANDARD; PRT; 223 AA.
AC P16410; O8WXJ1; Q96P43; Q9UKN9;
DT 01-AUG-1990 (Rel. 15, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Cytotoxic T-lymphocyte protein 4 precursor (Cytotoxic T-lymphocyte-associated antigen 4) (CTLA-4) (CD152 antigen).
GN CTLA4 OR CD152.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RX [1]
RA "SEQUENCE FROM N.A."
RA MEDLINE-21601151; PubMed-11735222;
RA Ling V., Wu P.W., Finnerty H.F., Agostino M.J., Graham J.R., Chen S., Jussif J., Fisk G.J., Miller C.P., Collins M.;
RT "Assembly and annotation of human chromosome 2q33 sequence containing the CD28, CTLA4, and ICOS gene cluster: analysis by computational, comparative, and microarray approaches.";
RT Genomics 78:155-168(2001).
RN [2]
RA "SEQUENCE FROM N.A."
RA Wu P.W., Ling V.;
RX "Full length sequence of hCTLA4 cDNA.";
RX Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.
RN [3]
RA "SEQUENCE OF 1-37 FROM N.A."
RA MEDLINE-91318145; PubMed-1713603;
RA Harper K., Balzano C., Rouvier E., Mattei M.-G., Luciani M.F., Golstein P.;
RX "CTLA-4 and CD28 activated lymphocyte molecules are closely related in both mouse and human as to sequence, message expression, gene structure, and chromosomal location.";
RX J. Immunol. 147:1037-1044(1991).
RN [4]
RA "SEQUENCE OF 38-223 FROM N.A."
RA TISSUE-Lymphocytes;
RX MEDLINE-99120925; PubMed-3220103;
RA Darivach P., Mattei M.-G., Golstein P., Lefranc M.-P.;
RX "Human Ig superfamily CTLA-4 gene: chromosomal localization and identity of protein sequence between murine and human CTLA-4 cytoplasmic domains.";
RX Eur. J. Immunol. 18:1901-1905(1988).
RN [5]
RA "SEQUENCE OF 140-223 FROM N.A., AND TISSUE SPECIFICITY."
RX MEDLINE-99425274; PubMed-10493833;
RA Ling V., Wu P.W., Finnerty H.F., Sharpe A.H., Gray G.S., Collins M.;
RX "Complete sequence determination of the mouse and human CTLA4 gene loci: cross-species DNA sequence similarity beyond exon borders.";
RX Genomics 60:341-355(1999).
RN [6]
RA FUNCTION.
RX MEDLINE-91341416; PubMed-1714933;

RA Linsley P.S., Brady W., Urnes M., Griesmaire L.S., Danie N.K.,
 RA Ledbetter J.A.: A second receptor for the B cell activation antigen B7.";
 RT "CTLA-4 is a second receptor for the B cell activation antigen B7.";
 RL J. Exp. Med. 174:561-569(1991).
 [7]
 RP STRUCTURE BY NMR OF 37-165.
 RX MEDLINE-97372889; PubMed-9228944;
 RA Metzger W.J., Bajorath J., Fenderson W., Shaw S.Y., Constantine K.L.,
 RA Nemer J., Leyte G., Peach R.J., Lavoie T.B., Mueller L.,
 RA Linsley P.S.;
 RT "Solution structure of human CTLA-4 and delineation of a CD80/CD86
 RT binding site conserved in CD28.";
 RL Nat. Struct. Biol. 4:527-531(1997).
 RN [8]
 RP VARIANT ALA-17, AND ASSOCIATION WITH IDDM2.
 RX MEDLINE-97402209; PubMed-9259273;
 RA Marion M.P., Raffel L.J., Gatchon H.-J., Jacob C.O., Serrano-Rios M.,
 RA Martinez Larrad M.T., Teng W.-P., Park Y., Zhang Z.-X.,
 RA Goldstein D.R., Tao Y.-W., Beaurain G., Bach J.-F., Huang H.-S.,
 RA Luo D.-F., Zeldner A., Rottler J.I., Yang M.C.K., Modilevsky T.,
 RA MacLaren N.K., She J.-X.;
 RT "Insulin-dependent diabetes mellitus (IDDM) is associated with CTLA4
 RT polymorphisms in multiple ethnic groups.";
 RL Hum. Mol. Genet. 6:1275-1282(1997).
 RN [9]
 RP POLYMORPHISM, AND ASSOCIATION WITH COELIAC DISEASE.
 RX MEDLINE-99205840; PubMed-10189842;
 RA Djilali-Saeh I., Schmitz J., Harfouch-Hammond E., Mougnot J.-F.,
 RA Bach J.-F., Caillat-Zucman S.;
 RT "CTLA-4 gene polymorphism is associated with predisposition to coeliac
 RT disease.";
 RL Gut 43:187-189(1998).
 RN [10]
 RP VARIANT ALA-17, AND ASSOCIATION WITH TAO.
 RX MEDLINE-99402177; PubMed-10475192;
 RA Valdiva B., Imrie H., Perros P., Dickinson J., McCarthy M.I.,
 RA Kendall-Taylor P., Pearce S.H.S.;
 RT "Cytotoxic T lymphocyte antigen-4 (CTLA-4) gene polymorphism confers
 RT susceptibility to thyroid associated orbitopathy.";
 RL Lancet 354:743-744(1999).
 RN [11]
 RP VARIANT ALA-17, AND ASSOCIATION WITH GRD.
 RX MEDLINE-20385252; PubMed-10924276;
 RA Chistyakov D.A., Savost'yanov K.V., Turakulov R.I., Petunina N.A.,
 RA Trukhina L.V., Kudanova A.V., Balabolkin M.I., Nosikov V.V.;
 RT "Complex association analysis of Graves disease using a set of
 RT polymorphic markers.";
 RL Mol. Genet. Metab. 70:214-218(2000).
 RN [12]
 RP VARIANT ALA-17.
 RX MEDLINE-20395844; PubMed-10903931;
 RA Deng Z., Morse J.H., Slager S.L., Cuervo N., Moore K.J., Venetos G.,
 RA Kalachikov S., Cayanis E., Fischer S.G., Barst R.J., Hodge S.E.,
 RA Knowles J.A.;
 RT "Familial primary pulmonary hypertension (gene PPH1) is caused by
 RT mutations in the bone morphogenetic protein receptor-II gene.";
 RL Am. J. Hum. Genet. 67:737-744(2000).
 CC -1- FUNCTION: POSSIBLY INVOLVED IN T-CELL ACTIVATION, BINDS TO B7-1
 CC (CD80) AND B7-2 (CD86).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Widely expressed with highest levels in
 CC lymphoid tissues.
 CC -1- POLYMORPHISM: The variant Ala-17 is associated with an increased
 CC risk for autoimmune disorders as Graves disease (GRD), type I
 CC insulin-dependent diabetes mellitus (IDDM12), and thyroid-
 CC associated orbitopathy (TAO). The variant Thr-17 is associated
 CC with predisposition to coeliac disease, a gluten sensitive
 CC enteropathy characterized by small bowel mucosal atrophy.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
 CC -1- DATABASE: NAME-PROT, NCBI-CD guide CD152 entry,
 CC WWW-http://www.ncbi.nlm.nih.gov/prov/CD/cd152.htm".
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL: AF411058; AAL04932.1; -;
 CC EMBL: AF411120; AAL07473.1; -;
 CC EMBL: M74363; AAA52127.1; -;
 CC EMBL: M37245; AAA52773.1; -;
 CC EMBL: M37243; AAA52773.1; JOINED.
 CC EMBL: M37244; AAA52773.1; JOINED.
 CC EMBL: AF142144; AAF02493.1; -;
 CC PIR: S08614; S08614.
 CC PDB: 1AH1; 15-APR-98.
 CC PDB: 1HEB; 28-NOV-01.
 CC PDB: 1I85; 04-APR-01.
 CC PDB: 1I8L; 04-APR-01.
 CC GeneW: HGNC:2505; CTLA4.
 CC MIM: 123890.
 CC GO: GO:0003687; C: Integral to plasma membrane; TAS.
 CC GO: GO:0006955; P: Immune response; TAS.
 CC InterPro: IPR003596; Ig_V.
 CC SMART: SM00409; Ig; 1.
 CC SMART: SM00406; IgV; 1.
 CC PROSITE: PS00835; IG_LIKE; FALSE_NEG.
 CC K1 Immunoglobulin domain; T-cell; Transmembrane; Glycoprotein; Signal;
 CC 3D-structure; Polymorphism.
 CC FT SIGNAL 1 35
 CC FT CHAIN 36 223
 CC FT DOMAIN 36 161
 CC FT TRANSMEM 162 187
 CC FT DOMAIN 188 223
 CC FT DOMAIN 39 140
 CC FT DISULFID 58 129
 CC FT CARBOHYD 85 103
 CC FT FT 113 113
 CC FT VARIANT 17 17
 CC FT N-LINKED (GLCNAC...) (POTENTIAL).
 CC FT T->A (in absnp:231775).
 CC FT /FTID-VAR 013577.
 CC FT T->A (in REF. 4).
 CC FT CONFLICT 147 147
 CC FT STRAND 45 47
 CC FT TURN 50 51
 CC FT STRAND 53 59
 CC FT STRAND 70 76
 CC FT STRAND 81 88
 CC FT TURN 91 92
 CC FT TURN 99 100
 CC FT STRAND 104 108
 CC FT TURN 109 110
 CC FT STRAND 111 117
 CC FT TURN 121 123
 CC FT STRAND 125 132
 CC FT TURN 137 138
 CC FT STRAND 142 143
 CC FT TURN 147 150
 CC FT SEQUENCE 223 AA; 24656 MW; 6F946FBE2E139A5A CRC64;
 CC
 CC Query Match 97.4%; Score 640; DB 1; Length 223;
 CC Best Local Similarity 98.4%; Pred. No. 6; 5e-59;
 CC Matches 133; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 CC
 CC QY 1 AMHVAPAVVLASSRGIASFVCEYASPGKTEVRVTLRQADSOVVECAATYMGNELT 60
 CC |
 CC DB 37 AMHVAPAVVLASSRGIASFVCEYASPGKTEVRVTLRQADSOVVECAATYMGNELT 96
 CC |
 CC QY 61 FLDDSTCTGTSSGNCQVNLITOGIRANDTGLYICKVELAMPYVEGIGNGTQIVYIDPP 120
 CC |
 CC DB 97 FLDDSTCTGTSSGNCQVNLITOGIRANDTGLYICKVELAMPYVEGIGNGTQIVYIDPP 156
 CC |
 CC QY 121 CPDSD 125
 CC |
 CC DB 157 CPDSD 161

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 23, 2003, 16:50:26 ; Search time 60 Seconds

(without alignments)
537.610 Million cell updates/sec

Title: US-09-865-321a-4_COPY_26_150

Perfect score: 657

Sequence: 1 AMHYAQAQPAVAVLASSRGIAASF.....GIGNGTQIVYIDPEPCPDSD 125

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 segs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacterioph:*

17: sp_archaeop:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	638	97.1	223	6	Q9BDG4
2	638	97.1	223	6	Q9BDN7
3	634	96.5	160	4	Q8TDA6
4	595	90.6	223	6	Q9BDP1
5	584	88.9	137	4	Q95653
6	579	88.1	115	4	Q9BZK2
7	564	85.8	223	6	Q9TWT2
8	564	85.8	223	6	Q9GKP2
9	561	85.4	223	11	Q9JLV3
10	560	85.2	223	6	Q9XTA1
11	560	85.2	223	6	Q9XSV7
12	550	83.7	223	6	Q9XST1
13	549	83.6	223	6	Q9N186
14	543	82.6	221	6	Q28050
15	530	80.7	221	6	Q97631
16	475	72.3	223	11	Q62859

17	420	63.9	174	11	Q9Z1A7	Q9Z1A7 rattus norv
18	252	38.4	68	11	Q99EP8	Q99EP8 cricetus
19	180	27.4	102	11	Q8CH94	Q8CH94 mus musculus
20	142	21.6	221	11	Q9JLV4	Q9JLV4 marmota mon
21	137	20.9	173	6	Q28289	Q28289 canis famli
22	137	20.9	221	6	Q9N0N8	Q9N0N8 canis famli
23	137	20.9	221	6	Q9GKP3	Q9GKP3 canis famli
24	133.5	20.3	219	6	Q97630	Q97630 ovis aries
25	133	20.2	221	6	Q02757	Q02757 felis silve
26	132	20.1	221	6	Q9N214	Q9N214 felis silve
27	130.5	19.9	220	6	Q9BDM6	Q9BDM6 macaca neme
28	129.5	19.7	138	6	Q8HYR9	Q8HYR9 bos taurus
29	129.5	19.7	220	6	Q9BDN5	Q9BDN5 cercopithec
30	128	19.5	220	6	Q9BDN2	Q9BDN2 callithrix
31	126.5	19.3	220	6	Q9BDN8	Q9BDN8 papio anubi
32	125.5	19.1	220	6	Q9BDM6	Q9BDM6 macaca mula
33	121	18.4	218	11	Q8CDB3	Q8CDB3 mus musculu
34	110	16.7	44	11	Q9Z1A8	Q9Z1A8 mus musculu
35	96	14.6	192	11	Q8CG11	Q8CG11 rattus norv
36	96	14.6	192	11	Q8CFD9	Q8CFD9 rattus norv
37	95	14.5	108	4	Q9UL79	Q9UL79 homo sapien
38	91.5	13.9	176	6	Q95JH8	Q95JH8 macaca fasc
39	91.5	13.9	180	6	Q8MJ02	Q8MJ02 macaca mula
40	90.5	13.8	51	6	Q8MIS6	Q8MIS6 bos taurus
41	90.5	13.8	235	11	Q91W12	Q91W12 mus musculu
42	88.5	13.5	177	4	Q14930	Q14930 homo sapien
43	88.5	13.5	190	4	Q14932	Q14932 homo sapien
44	88.5	13.5	201	4	Q14931	Q14931 homo sapien
45	86	13.1	151	6	Q8MJ01	Q8MJ01 macaca mula

ALIGNMENTS

RESULT 1	ID	Q9BDG4	PRELIMINARY:	PRT:	223 AA.
AC	Q9BDG4	01-JUN-2001 (TREMBLrel. 17, Created)			
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)				
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)				
DE	CD152 protein precursor.				
CN	CTA-4				
OS	Macaca mulatta (Rhesus macaque),				
OS	Macaca nemestrina (Pig-tailed macaque), and				
OS	Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).				
CC	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;				
CC	Mammalia: Eutheria: Primates: Catarrhini: Cercopithecoidea;				
CC	Cercopithecoidea: Macaca.				
OX	NCBI_TaxID=9544, 9545, 9531;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	SPECIES=M.mulatta, M.nemestrina, and C.torquatus atys;				
RA	Villinger F., Bostlik P., Mayne A.E., King C.L., Genain C.P.,				
RT	Weiss W.R., Ansari A.A.;				
RT	"Cloning, sequencing and co-stimulatory molecules."				
RT	Fas/Fas-ligand and co-stimulatory molecules."				
RL	Immunogenetics 0:0-0(2001).				
DR	EMBL: AF344846; AKK37605.1;				
DR	EMBL: AF344854; AKK37537.1;				
DR	EMBL: AF344848; AKK37608.1;				
DR	HSSP: P16410; IAH1.				
DR	InterPro: IPR003596; Iq_v.				
DR	SMART: SMO0406; IGV; I.				
KW	SIGNAL.				
FT	SIGNAL.				
FT	VARIANT	1	37	POTENTIAL.	
SO	SEQUENCE	223	223	N->D.	
		223	24683	MM: BDE42248A00398FA	CRC64;
	Query Match	97.1%	Score 638;	DB 6;	Length 223;
	Best Local Similarity	97.6%	Pred. No. 8.7e-61;		
	Matches 122;	Conservative 1;	Mismatches 2;	Gaps 0;	

QY 1 AMHVAPAVVLASSRGISAFVCEYASPGKTEVRVTVLRQADSOVTEVCAATYMMGNELT 60
 DB 37 AMHVAPAVVLASSRGISAFVCEYASPGKATEVRVTVLRQADSOVTEVCAATYMMGNELT 96
 QY 61 FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMPPPYEGISNGTOIYIDPEP 120
 DB 97 FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMPPPYMGISNGTOIYIDPEP 156
 QY 121 CPDSD 125
 DB 157 CPDSD 161

RESULT 2

Q9BDN7 PRELIMINARY; PRT; 223 AA.

ID Q9BDN7
 AC Q9BDN7
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE CD152 protein precursor.
 GN CTLA-4.
 OS Papio anubis (Olive baboon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
 OC Cercopitheciinae; Papio.
 OX NCBI_TaxID=9555;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-21383618; PubMed-11491535;
 RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
 RA Weiss W.R., Ansari A.A.;
 RT "Cloning, sequencing, and homology analysis of nonhuman primate
 Fas/Fas-1 ligand and co-stimulatory molecules.";
 RL EMBL; AF344838; AAK37534.1; -
 RL EMBL; AF344838; AAK37534.1; -
 DR HSSP; P16410; IAH1.
 DR InterPro: IPR003596; Ig-V.
 DR SMART; SM00406; IGV; 1.
 KW Signal.
 FT SIGNAL.
 SQ SEQUENCE 223 AA; 24655 MW; EC18C279CCCC5668 CRC64;

Query Match 97.1%; Score 638; DB 6; Length 223;
 Best Local Similarity 97.6%; Pred. No. 8.7e-61;
 Matches 122; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 AMHVAPAVVLASSRGISAFVCEYASPGKTEVRVTVLRQADSOVTEVCAATYMMGNELT 60
 DB 37 AMHVAPAVVLASSRGISAFVCEYASPGKATEVRVTVLRQADSOVTEVCAATYMMGNELT 96
 QY 61 FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMPPPYEGISNGTOIYIDPEP 120
 DB 97 FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMPPPYMGISNGTOIYIDPEP 156
 QY 121 CPDSD 125
 DB 157 CPDSD 161

RESULT 3

Q8TDAG PRELIMINARY; PRT; 160 AA.

ID Q8TDAG
 AC Q8TDAG
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE CT1A4 (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiinae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]

RP SEQUENCE FROM N.A.
 RA Guo J.H., Fan M.W., Bian Z., Jia R.;
 RT "Partial sequence of CT1A4 mRNA, signal peptide and extracellular
 RT domain.";
 RT Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF486806; AAL9664.1; -
 DR InterPro: IPR003596; Ig-V.
 DR SMART; SM00406; IGV; 1.
 FT NON_TER 160
 SQ SEQUENCE 160 AA; 17470 MW; 1385B4644F63836F CRC64;

Query Match 96.5%; Score 634; DB 4; Length 160;
 Best Local Similarity 98.4%; Pred. No. 1.5e-60;
 Matches 122; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AMHVAPAVVLASSRGISAFVCEYASPGKTEVRVTVLRQADSOVTEVCAATYMMGNELT 60
 DB 37 AMHVAPAVVLASSRGISAFVCEYASPGKATEVRVTVLRQADSOVTEVCAATYMMGNELT 96
 QY 61 FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMPPPYEGISNGTOIYIDPEP 120
 DB 97 FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMPPPYMGISNGTOIYIDPEP 156
 QY 121 CPDSD 124
 DB 157 CPDSD 160

RESULT 4

Q9BDP1 PRELIMINARY; PRT; 223 AA.

ID Q9BDP1
 AC Q9BDP1
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE CD152 protein precursor.
 GN CTLA-4.
 OS Aotus trivirgatus (Night monkey) (Douroucoul).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
 OX NCBI_TaxID=9505;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-21383618; PubMed-11491535;
 RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
 RA Weiss W.R., Ansari A.A.;
 RT "Cloning, sequencing, and homology analysis of nonhuman primate
 Fas/Fas-1 ligand and co-stimulatory molecules.";
 RL EMBL; AF344834; AAK37530.1; -
 RL EMBL; AF344834; AAK37530.1; -
 DR HSSP; P16410; IAH1.
 DR InterPro: IPR003599; Ig.
 DR SMART; SM00409; IGV; 1.
 KW Signal.
 FT SIGNAL.
 SQ SEQUENCE 223 AA; 24813 MW; 3F702052117C1431 CRC64;

Query Match 90.6%; Score 595; DB 6; Length 223;
 Best Local Similarity 90.4%; Pred. No. 3.8e-56;
 Matches 113; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 AMHVAPAVVLASSRGISAFVCEYASPGKTEVRVTVLRQADSOVTEVCAATYMMGNELT 60
 DB 37 AMHVAPAVVLASSRGISAFVCEYASPGKATEVRVTVLRQADSOVTEVCAATYMMGNELT 96
 QY 61 FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMPPPYEGISNGTOIYIDPEP 120
 DB 97 FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMPPPYMGISNGTOIYIDPEP 156
 QY 121 CPDSD 125
 DB 157 CPDSD 161

GenCore version 5.1.6.
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 23, 2003, 16:43:01 ; Search time 60.5 Seconds

(without alignments)
327,947 Million cell updates/sec

Title: US-09-865-321A-4_COPY_26_150

Sequence: 1 AMHVAPAVVLASSRGIAF.....GICNGIOIYIDPEPCDSD 125

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /Geneseq_19Jun03: *
2: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1980.DAT: *
3: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT: *
4: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1982.DAT: *
5: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1983.DAT: *
6: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1984.DAT: *
7: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1985.DAT: *
8: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1986.DAT: *
9: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1987.DAT: *
10: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1988.DAT: *
11: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1989.DAT: *
12: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1990.DAT: *
13: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1991.DAT: *
14: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1992.DAT: *
15: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1993.DAT: *
16: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1994.DAT: *
17: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1995.DAT: *
18: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1996.DAT: *
19: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1997.DAT: *
20: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1998.DAT: *
21: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1999.DAT: *
22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2000.DAT: *
23: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT: *
24: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2002.DAT: *
25: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2003.DAT: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	657	100.0	383	23	ABB78102
2	657	100.0	383	23	AAAM50654
3	657	100.0	383	23	AAU75120
4	657	100.0	383	23	AAAB47862
5	657	100.0	383	24	ABP56717
6	652	99.2	383	23	ABB78105
7	652	99.2	383	23	AAU75123
8	652	99.2	383	24	ABP56721
9	649	98.8	212	23	AAU75127

10	649	98.8	212	23	AAU75132	Human CTLA4 recept
11	649	98.8	383	23	ABB78103	Amino acid sequenc
12	649	98.8	383	23	AAU75121	Human soluble CTLA
13	649	98.8	383	24	ABP56719	CTLA4 mutant L104E
14	648	98.6	212	23	AAU75131	Human CTLA4 recept
15	648	98.6	383	23	ABB78101	Amino acid sequenc
16	648	98.6	383	23	AAAB50655	Soluble CTLA4 muta
17	648	98.6	383	23	AAU75119	Human soluble CTLA
18	648	98.6	383	23	AAU75122	Human soluble CTLA
19	648	98.6	383	24	ABP56718	CTLA4 mutant L104E
20	648	98.6	383	24	ABP56720	CTLA4 mutant L104E
21	644	98.0	212	23	AAU75129	Human CTLA4 recept
22	643	97.9	212	23	AAU75130	Human CTLA4 recept
23	643	97.9	212	23	AAU75126	Human CTLA4 recept
24	641	97.6	212	23	AAU75128	Human CTLA4 recept
25	640	97.4	187	20	AAV41130	CTLA4 receptor wit
26	640	97.4	187	20	AAW97615	Human CTLA recepto
27	640	97.4	187	20	AAW97610	Human CTLA recepto
28	640	97.4	187	20	AAW97560	Human CTLA4 recept
29	640	97.4	211	20	AAW8106	Human CTLA4 recept
30	640	97.4	212	15	AAW8104	Human CTLA4 recept
31	640	97.4	212	15	AAW8104	Human CTLA4 recept
32	640	97.4	212	16	AAW8104	Human CTLA4 recept
33	640	97.4	212	20	AAW8104	Human CTLA4 recept
34	640	97.4	212	20	AAW8104	Human CTLA4 recept
35	640	97.4	212	23	AAW8106	Amino acid sequenc
36	640	97.4	212	23	AAU75124	Amino acid sequenc
37	640	97.4	212	24	ABP56715	Human CTLA4 recept
38	640	97.4	223	21	AAV15129	Human CTLA-4 prote
39	640	97.4	223	23	AAU74508	Human cytotoxic T-
40	640	97.4	223	23	AAU74508	Human cytotoxic T-
41	640	97.4	364	21	AAV93688	Fusion protein of
42	640	97.4	374	18	AAW26206	CTLA4-1964 fusion
43	640	97.4	374	18	AAW26207	CTLA4-modified IgG
44	640	97.4	377	18	AAW26208	CTLA4-modified IgG
45	640	97.4	383	23	ABB78107	Amino acid sequenc

ALIGNMENTS

RESULT 1
ABB78102
ID ABB78102 standard; Protein: 383 AA.
XX
AC ABB78102;
XX
DT 05-NOV-2002 (first entry)
XX
DE Amino acid sequence of a CTLA4Ig mutant, designated L104EA29Yig.
XX
KW CTLA4Ig; mutant; L104EA29Yig; CTLA4; immunoglobulin; Ig; B7;
KW immunosuppressive; mixed haematopoietic chimerism; transplanted tissue;
KW T cell depleted bone marrow cell; T cell costimulatory signal;
KW haemoglobinopathy; beta-thalassemia; sickle cell disease;
KW organ rejection.
XX
OS Synthetic.
XX
PN WO200258729-A2.
XX
PD 01-AUG-2002.
XX
PE 25-JAN-2002; 2002WO-US03780.
XX
PR 26-JAN-2001; 2001US-264528P.
XX
PR 05-JUL-2001; 2001US-303142P.
XX
PA (UYEM-) UNIV EMORY.
XX
PI Larsen CP, Pearson TC, Waller EK, Adams AB;
XX
DR WPI, 2002-619143/66.

XX Establishing mixed hematopoietic chimerism in subject after
PT transplantation, by administering T cell depleted bone marrow cells,
PT alkylating agent, immunosuppressive composition that blocks T cell
PT costimulatory signals -
XX
PS Example 8; Fig 15; 16pp; English.
XX
XX The present sequence represents a CTLA4lg mutant, designated L104EA29Ylg.
CC CTLA4lg is a soluble fusion protein, comprising an extracellular domain
CC of wild type CTLA4 joined to an immunoglobulin (Ig) tail or a portion
CC thereof which binds a B7 molecule. The present protein has the mutations
CC A29Y and L104E. CTLA4lg and its mutants are examples of immunosuppressive
CC agents that may be used in the method of the invention. The specification
CC describes a method of establishing mixed hematopoietic chimerism in
CC a subject with a transplanted tissue. The method comprises administering
CC to the subject, T cell depleted bone marrow cells, an alkylating agent
CC and an immunosuppressive composition that blocks T cell costimulatory
CC signals in the subject, thus establishing hematopoietic chimerism in the
CC subject. The method is useful for treating hematopoietic chimerism in the
CC (e.g. beta-thalassemia or sickle cell disease), in a subject by
CC establishing hematopoietic chimerism. It is also useful for inhibiting
CC rejection of an organ or tissue transplanted into the subject.
XX
SQ Sequence 383 AA:
Query Match 100.0%; Score 657; DB 23; Length 383;
Best Local Similarity 100.0%; Pred. No. 1.8e-58;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AMHVAQPAVAVLASSRGIAFVCEYASPGKTEYEVTVLRQADSOVTEVCATYMGNELT 60
DB 26 AMHVAQPAVAVLASSRGIAFVCEYASPGKTEYEVTVLRQADSOVTEVCATYMGNELT 85
QY 61 FLDDSLCTGTSSNGVNLITGGIRAMDGTGTYCKVELMTPPYEGIGNTQIYVDDPEP 120
DB 86 FLDDSLCTGTSSNGVNLITGGIRAMDGTGTYCKVELMTPPYEGIGNTQIYVDDPEP 145
QY 121 CPDSD 125
DB 146 CPDSD 150

RESULT 2
AA050654
AA050654 standard; Protein: 383 AA.
XX
AC AA050654;
XX
DT 04-APR-2002 (first entry)
XX
DE Soluble CTLA4 mutant L104EA29Ylg.
XX
XX CTLA4; cytotoxic T-lymphocyte associated antigen-4; L104EA29Ylg;
KW graft versus host disease; psoriasis; diabetes; immunosuppressive;
KW antihypertensive; antidiabetic; thyromimetic; antidiabetic;
KW antitumor; dermatological; antineoplastic; antidiabetic;
KW nephrotoxic; neuroprotective; ophthalmological; antirheumatic;
KW antitachycardic; antipsoriatic; antitumor; therapy; human; antibody;
KW immunoglobulin; mutant; mutagen.
XX
XX Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..26
FT Protein /label= signal_peptide
FT Protein /label= Mature_protein
FT Region 27..150
FT Region /label= CTLA4
FT Region 152..383
FT Region /label= Immunoglobulin

XX
PN WO200192337-A2.
XX
XX 06-DEC-2001.
XX
PD 23-MAY-2001; 2001WO-US17139.
PF
PE 26-MAY-2000; 2000US-0579927.
XX 26-JUN-2000; 2000US-214065P.
XX
XX (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
XX Peach RJ, Naemura JR, Linsley PS, Bajorath J;
DR MPI: 2002-130525/17.
XX N-PSDB; AAI71098.
XX
XX Novel mutant cytotoxic T-lymphocyte-associated antigen-4 molecule which
PT binds CD80 and/or CD86 with greater avidity than wild-type molecule, is
PT useful for inhibiting graft versus host disease, psoriasis and diabetes
PT
XX
XX Claim 6; Fig 7; 64pp; English.
XX
XX The present sequence is that of a novel, soluble cytotoxic
CC T-lymphocyte-associated antigen-4 (CTLA4) mutant, designated
CC L104EA29Ylg, in which amino acids 1-124 of the mature protein
CC comprise the CTLA4 extracellular portion and amino acids 126-357
CC comprise the immunoglobulin portion. The amino acid sequence of
CC L104EA29Ylg can begin with alanine at amino acid position -1 or
CC methionine at position +1, and ends with lysine at position +357.
CC Compared with non-mutated CTLA4lg, L104EA29Ylg has tyrosine
CC replacing alanine at position +29 instead of alanine, and glutamic
CC acid replacing leucine at position +101. Mutations were introduced
CC into CTLA4lg DNA by PCR primer-directed mutagenesis. A single
CC mutant was initially generated, and used as template to generate
CC the double mutant. Host-vector systems are claimed where the host
CC is especially a COS or CHO cell. L104EA29Ylg binds approximately
CC 2-fold more avidly than wild-type CTLA4lg to CD80 and approximately
CC 4-fold more avidly to CD86, making it more effective than CTLA4lg at
CC blocking immune responses. L104EA29Ylg is a claimed example of novel,
CC soluble CTLA4 mutant molecules of the invention that recognise and
CC bind CD80 and/or CD86. These are useful for inhibiting interaction
CC between the CTLA4-positive T-cells and CD80 and CD86 positive cells.
CC They are also useful for treating immune system diseases mediated by
CC T-cell interactions with CD80 and/or CD86 positive cells by
CC regulating T-cell interactions with the CD80 and/or CD86 positive
CC cells. When used with a ligand reactive with interleukin-4, they
CC are useful for inhibiting graft versus host disease (all claimed).
CC The mutant soluble CTLA4 molecules are also useful for downregulating
CC immune responses by inhibiting the functions of activated T-cells,
CC such as a T-lymphocyte proliferation and cytokine secretion by
CC suppressing T-cell responses or by inducing specific tolerance in
CC T-cells or both, for treating immune system diseases mediated by
CC CD28- and/or CTLA4-positive cell interactions, such as autoimmune
CC diseases (lupus, Hashimoto's thyroiditis, primary myxedema, Grave's
CC disease, pernicious anaemia, diabetes, Goodpasture's syndrome,
CC Crohn's disease, multiple sclerosis, autoimmune uveitis, rheumatoid
CC arthritis, scleroderma, etc.), immunoproliferative diseases
CC (psoriasis, T-cell lymphoma, T-cell acute lymphoblastic leukaemia,
CC etc.), and graft related disorders (graft versus host disease,
CC immune disorders associated with graft transplantation rejection,
CC chronic rejection, etc.), for inhibiting solid organ and/or tissue
CC transplant rejection, and for treating autoimmune disorders by
CC preventing activation of autoreactive T-cells.
XX
XX
SQ Sequence 383 AA:
Query Match 100.0%; Score 657; DB 23; Length 383;
Best Local Similarity 100.0%; Pred. No. 1.8e-58;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AMHVAQPAVAVLASSRGIAFVCEYASPGKTEYEVTVLRQADSOVTEVCATYMGNELT 60

```

DB 26 AMHVAQPAVVLASSRGIAFVCEYASPKYTEVRVTYLRQDSQVTEVCATYMMGNELT 85
OY 61 FLDDSICTGTSSGNQVNLITIGLRAMDGTLYICKVELMPPPYEGIGNGTQIYIDPEP 120
DB 86 FLDDSICTGTSSGNQVNLITIGLRAMDGTLYICKVELMPPPYEGIGNGTQIYIDPEP 145
OY 121 CPDSD 125
DB 146 CPDSD 150

RESULT 3
AAU75120
ID AAU75120 standard; Protein: 383 AA.
XX
AC AAU75120;
XX
DT 09-APR-2002 (first entry)
XX
DE Human soluble CTLA4 mutant protein, L104EA29Yig.
XX
KW Human; rheumatic disease; soluble cytotoxic T lymphocyte antigen 4; Ig;
KW CTLA4; variable (V)-like extracellular domain; CTLA4ig; B7 molecule;
KW immunoglobulin constant domain; rheumatoid arthritis; autoimmune disease;
KW immune system disorder; graft-related disease; immunosuppressive; mutant;
KW immunoproliferative disease; antiinflammatory; mutant; L104EA29Yig.
XX
OS Homo sapiens.
XX
FH Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..26
FT /label= Signal_peptide
FT Protein 27..383
FT /label= Mature_L104EA29Yig-mutant
FT MISC-difference 55
FT /note= "Substitution of wild type Ala to Tyr"
FT MISC-difference 130
FT /note= "Substitution of wild type Leu to Glu"
XX
PN WO200202638-A2.
XX
PD 10-JAN-2002.
XX
PF 02-JUL-2001; 2001WO-US21204.
XX
PR 03-JUL-2000; 2000US-215913P.
XX
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
PI Cohen R, Carr S, Hagerly D, Peach RJ, Becker J;
XX
DR WPI; 2002-148002/19.
XX
DR N-PSDB; AAS20942.
XX
XX
XX Composition useful for treating rheumatic disease and immune system
XX disorders e.g. diabetes mellitus, graft-related disease, good pasture's
XX syndrome, comprises soluble cytotoxic T lymphocyte A4 mutant molecule
XX
XX Claim 9; Fig 19; 128pp; English.
XX
XX The present invention relates to pharmaceutical compositions and
XX methods for treating rheumatic disease. The composition comprises a
XX soluble cytotoxic T lymphocyte antigen 4 (CTLA4) mutant molecule that
XX blocks endogenous B7 molecules from binding their ligands. Soluble
XX CTLA4 molecules are constructed by fusing variable (V)-like
XX extracellular domains of CTLA4 to immunoglobulin (Ig) constant domains
XX resulting in CTLA4ig. The composition is useful for treating rheumatic
XX disease especially rheumatoid arthritis, and for alleviating a symptom
XX associated with a rheumatic disease from joint swelling, pain,
XX tenderness, and structural damage. The composition can optionally be used

```

```

CC with other pharmaceutical agents for treating immune system disorders
CC which include autoimmune diseases (e.g. systemic lupus erythematosus,
CC Addison's disease, diabetes mellitus, multiple sclerosis, Crohn's
CC disease, ulcerative colitis, Sjogren's syndrome, scleroderma and
CC sympathetic ophthalmia), graft-related diseases (e.g. graft-versus-host
CC disease), immunoproliferative diseases (e.g. psoriasis, T cell lymphoma,
CC Hashimoto's thyroiditis, pernicious anaemia and good pasture's syndrome).
CC The present sequence represents human soluble CTLA4 mutant protein,
CC L104EA29Yig.
XX
SQ Sequence 383 AA;
XX
OY Query Match 100.0%; Score 657; DB 23; Length 383;
DB Best Local Similarity 100.0%; Pred. No. 1.8e-58;
DB Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 AMHVAQPAVVLASSRGIAFVCEYASPKYTEVRVTYLRQDSQVTEVCATYMMGNELT 60
DB 26 AMHVAQPAVVLASSRGIAFVCEYASPKYTEVRVTYLRQDSQVTEVCATYMMGNELT 85
OY 61 FLDDSICTGTSSGNQVNLITIGLRAMDGTLYICKVELMPPPYEGIGNGTQIYIDPEP 120
DB 86 FLDDSICTGTSSGNQVNLITIGLRAMDGTLYICKVELMPPPYEGIGNGTQIYIDPEP 145
OY 121 CPDSD 125
DB 146 CPDSD 150

RESULT 4
AAB47862
ID AAB47862 standard; Protein: 383 AA.
XX
AC AAB47862;
XX
DT 15-APR-2002 (first entry)
XX
DE Human L104EA29Yig.
XX
KW Human; soluble; CTLA4; CTLA4ig; L104EA29Yig; pharmaceutical; CD28; ape;
KW B7; CD40; CD154; adhesion molecule; LFA-1; ICAM-2; ICAM-3; dog;
KW alpha-actinin; filamin; cytohesin-1; immune system; myasthenia gravis;
KW graft versus host disease; psoriasis; graft transplant rejection; rat;
KW testicular angiocentric T cell lymphoma; benign lymphocytic angitis;
KW lupus; lupus erythematosus; lupus nephritis; Hashimoto's thyroiditis;
KW primary myxedema; Graves' disease; pernicious anaemia; Crohn's disease;
KW autoimmune atrophic gastritis; Addison's disease; diabetes; pemphigus;
KW insulin dependent diabetes mellitus; type I diabetes mellitus; rabbit;
KW good pasture's syndrome; T cell acute lymphoblastic leukemia; cat; cow;
KW sympathetic ophthalmia; autoimmune uveitis; multiple sclerosis; mouse;
KW autoimmune haemolytic anaemia; idiopathic thrombocytopenia; scleroderma;
KW primary biliary cirrhosis; chronic action hepatitis; ulcerative colitis;
KW Sjogren's syndrome; rheumatoid arthritis; polymyositis; T cell lymphoma;
KW human; monkey; horse.
XX
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX FH Peptide 1..26
XX FT /label= Oncostatin_signal_peptide
XX FT Protein 27..383
XX FT /label= L104EA29Yig
XX
XX WO200195928-A2.
XX
XX 20-DEC-2001.
XX
XX 08-JUN-2001; 2001WO-US18619.
XX
XX 09-JUN-2000; 2000US-210671P.
XX
XX (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX

```


RESULT 6
 ID ABB78105 standard; Protein: 383 AA.
 XX ABB78105;
 XX
 DT 05-NOV-2002 (first entry)
 XX
 DE Amino acid sequence of a CTLA4lg mutant, designated L104EA29Wlg.
 XX
 KW CTLA4lg; mutant; L104EA29Wlg; CTLA4; immunoglobulin; Ig; B7;
 KW immunosuppressive; mixed haematopoietic chimerism; transplanted tissue;
 KW T cell depleted bone marrow cell; T cell costimulatory signal;
 KW haemoglobinopathy; beta-thalassemia; sickle cell disease;
 KW organ rejection.
 XX
 OS Synthetic.
 XX
 PN W0200258729-A2.
 XX
 PD 01-AUG-2002.
 XX
 PF 25-JAN-2002; 2002WO-US03780.
 XX
 PR 26-JAN-2001; 2001US-264528P.
 XX
 PR 05-JUL-2001; 2001US-303142P.
 XX
 PA (UYEM-) UNIV EMORY.
 XX
 PI Larsen CP, Pearson TC, Waller EK, Adams AB;
 XX
 DR WPI; 2002-619143/66.
 DR N-PSDB; ABO78360.
 XX
 PT Establishing mixed haematopoietic chimerism in subject after
 PT transplantation, by administering T cell depleted bone marrow cells,
 PT alkylating agent, immunosuppressive composition that blocks T cell
 PT costimulatory signals -
 XX
 PS Example 8; Fig 18; 161pp; English.
 XX
 CC The present sequence represents a CTLA4lg mutant, designated L104EA29Wlg.
 CC CTLA4lg is a soluble fusion protein, comprising an extracellular domain
 CC of wild type CTLA4 joined to an immunoglobulin (Ig) tail or a portion
 CC thereof which binds a B7 molecule. The present protein has the mutations
 CC A29W and L104E. CTLA4lg and its mutants are examples of immunosuppressive
 CC agents that may be used in the method of the invention. The specification
 CC describes a method of establishing mixed haematopoietic chimerism in
 CC a subject with a transplanted tissue. The method comprises administering
 CC to the subject, T cell depleted bone marrow cells, an alkylating agent
 CC and an immunosuppressive composition that blocks T cell costimulatory
 CC signals in the subject, thus establishing haematopoietic chimerism in the
 CC subject. The method is useful for treating haemoglobinopathy
 CC (e.g. beta-thalassemia or sickle cell disease), in a subject by
 CC establishing haematopoietic chimerism. It is also useful for inhibiting
 CC rejection of an organ or tissue transplanted into the subject.
 CC
 SQ Sequence 383 AA;
 XX
 Query March 99.2%; Score 652; DB 23; Length 383;
 Best Local Similarity 99.2%; Pred. No. 5.8e-58;
 Matches 124; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AMHVAQPAVYVLAASSRGIAIFVCEYASPGKYTEFRTVYROADSQTVEVCATYMMGNLIT 60
 Db 26 AMHVAQPAVYVLAASSRGIAIFVCEYASPGKYTEFRTVYROADSQTVEVCATYMMGNLIT 85
 QY 61 FLDDSICTGSSGNQVNLITIGLRAMDGLTYCKVELMPPPYEGIGNGTQIYIDEP 120
 Db 86 FLDDSICTGSSGNQVNLITIGLRAMDGLTYCKVELMPPPYEGIGNGTQIYIDEP 145

QY 121 CPDSD 125
 Db 146 CPDSD 150
 RESULT 7
 ID AAU75123 standard; Protein: 383 AA.
 XX AAU75123;
 XX
 DT 09-APR-2002 (first entry)
 XX
 DE Human soluble CTLA4 mutant protein, L104EA29Wlg.
 XX
 KW Human; rheumatic disease; soluble cytotoxic T lymphocyte antigen 4; Ig;
 KW CTLA4; variable (V)-like extracellular domain; CTLA4lg; B7 molecule;
 KW immunoglobulin constant domain; rheumatoid arthritis; autoimmune disease;
 KW immune system disorder; graft-related disease; immunosuppressive; mutant;
 KW immunoproliferative disease; antinflammatory; mutant; L104EA29Wlg.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 EH Key Location/Qualifiers
 FT Peptide 1..26
 FT Protein /label= Signal_peptide
 FT /label= Mature_L104EA29Wlg-mutant
 FT MISC-difference 55
 FT /note= "Substitution of wild type Ala to Trp"
 FT MISC-difference 130
 FT /note= "Substitution of wild type Leu to Glu"
 XX
 PN W0200202638-A2.
 XX
 PD 10-JAN-2002.
 XX
 PF 02-JUL-2001; 2001WO-US21204.
 XX
 PR 03-JUL-2000; 2000US-215913P.
 XX
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX
 PI Cohen R, Carr S, Hagerly D, Peach RJ, Becker J;
 XX
 DR WPI; 2002-148002/19.
 DR N-PSDB; AAS20945.
 XX
 PT Composition useful for treating rheumatic disease and immune system
 PT disorders e.g. diabetes mellitus, graft-related disease, good pasture's
 PT syndrome, comprises soluble cytotoxic T lymphocyte A4 mutant molecule
 XX
 PS Claim 9; Fig 22; 128pp; English.
 XX
 CC The present invention relates to pharmaceutical compositions and
 CC methods for treating rheumatic disease. The composition comprises a
 CC soluble cytotoxic T lymphocyte antigen 4 (CTLA4) mutant molecule that
 CC blocks endogenous B7 molecules from binding their ligands. Soluble
 CC CTLA4 molecules are constructed by fusing variable (V)-like
 CC extracellular domains of CTLA4 to immunoglobulin (Ig) constant domains
 CC resulting in CTLA4lg. The composition is useful for treating rheumatic
 CC disease especially rheumatoid arthritis, and for alleviating a symptom
 CC associated with a rheumatic disease from joint swelling, pain,
 CC tenderness, and structural damage. The composition can optionally be used
 CC with other pharmaceutical agents for treating immune system disorders
 CC which include autoimmune diseases (e.g. systemic lupus erythematosus,
 CC Addison's disease, diabetes mellitus, multiple sclerosis, Crohn's
 CC disease, ulcerative colitis, Sjogren's syndrome, scleroderma and
 CC sympathetic ophthalmia), graft-related diseases (e.g. graft-versus-host
 CC disease), immunoproliferative diseases (e.g. psoriasis, T cell lymphoma,
 CC Hashimoto's thyroiditis, pernicious anaemia and good pasture's syndrome).

CC The present sequence represents human soluble CTLA4 mutant protein,
 CC L104EA29W1g.
 XX
 SQ Sequence 383 AA;
 Query Match 99.2%; Score 652; DB 23; Length 383;
 Best Local Similarity 99.2%; Pred. No. 5.8e-58;
 Matches 124; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AMHVAQPAVYVLAASRGIAFVCEASPGKTEVRVYVLRQADSOVTEVCATYMGNELT 60
 DB 26 AMHVAQPAVYVLAASRGIAFVCEASPGKTEVRVYVLRQADSOVTEVCATYMGNELT 85
 QY 61 FLDDSTCTGSSGNQVNLITQGLRAMDTGLYICKVELMPPPYEGIGNGTQIVIDPEP 120
 DB 86 FLDDSTCTGSSGNQVNLITQGLRAMDTGLYICKVELMPPPYEGIGNGTQIVIDPEP 145
 QY 121 CPDSD 125
 DB 146 CPDSD 150
 RESULT 8
 ABP56721 ID ABP56721 standard; Protein: 383 AA.
 XX
 AC ABP56721;
 DT 27-MAR-2003 (first entry)
 XX
 DE CTLA4 mutant L104EA29W1g protein SEQ ID NO:14.
 XX
 KW CTLA4; mutant; islet cell transplantation rejection inhibition;
 KW cytotoxic T lymphocyte associated antigen-4; antidiabetic; antithyroid;
 KW immunoprotective; neutropenic; dermatological; antipsoriatic;
 KW diabetes; immune system disease; psoriasis; Graves' disease;
 KW multiple sclerosis; oncostatin.
 XX
 OS Homo sapiens.
 OS Synthetic.
 OS
 FH Key Location/Qualifiers
 FT Peptide 1..26
 FT Protein /label= oncostatin_signal_peptide
 FT 27..383
 FT /label= CTLA4_mutant_L104EA29W1g
 XX
 PN W0200294202-A2.
 XX
 PD 28-NOV-2002.
 XX
 PE 23-MAY-2002; 2002WO-US16708.
 XX
 PR 23-MAY-2001; 2001US-293402P.
 XX
 PA (UYEM-) UNIV EMORY.
 XX
 PI Larsen CP, Pearson TC, Adams AB;
 XX
 DR WPI: 2003-140318/13.
 DR N-PSDB; ABZ22588.
 XX
 PT Inhibiting islet cell transplant rejection in a subject, useful for
 PT treating diabetes by administering a cytotoxic T lymphocyte associated
 PT antigen-4 mutant molecule
 PS Claim 2; Fig 20; 100pp; English.
 CC The present invention describes a method of inhibiting islet cell
 CC transplantation rejection in a subject comprising administering a
 CC cytotoxic T lymphocyte associated antigen-4 (CTLA-4) mutant (soluble)
 CC molecule (I), where the subject is transplanted with islet cells before,
 CC or after administration of (I). (I) has antidiabetic, immunoprotective,

CC neuroprotective, dermatological, antipsoriatic and antithyroid
 CC activities. (I) can be used for inhibiting islet cell transplant
 CC rejection in a subject e.g. a human, non-human primate (preferably
 CC monkey), rabbit, sheep, rat, dog, cat, pig or mouse. The method is useful
 CC for treating diabetes. (I) is also useful for treating immune system
 CC diseases e.g. psoriasis, Graves' disease and multiple sclerosis. The
 CC method provides a novel calcineurin inhibitor/steroid-free
 CC immunosuppressive regimen that provides significant protection from
 CC rejection and prolongs the survival of islet allografts in nonhuman
 CC primates. The agent L104EA29W1g is a potent immunosuppressant, and so
 CC replaces tacrolimus in the Edmonton protocol, thereby eliminating the
 CC unwanted side effects of the calcineurin inhibitor. The present sequence
 CC represents a CTLA4 mutant L104EA29W1g protein, which is used in an
 CC example from the present invention.
 XX
 SQ Sequence 383 AA;
 Query Match 99.2%; Score 652; DB 24; Length 383;
 Best Local Similarity 99.2%; Pred. No. 5.8e-58;
 Matches 124; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AMHVAQPAVYVLAASRGIAFVCEASPGKTEVRVYVLRQADSOVTEVCATYMGNELT 60
 DB 26 AMHVAQPAVYVLAASRGIAFVCEASPGKTEVRVYVLRQADSOVTEVCATYMGNELT 85
 QY 61 FLDDSTCTGSSGNQVNLITQGLRAMDTGLYICKVELMPPPYEGIGNGTQIVIDPEP 120
 DB 86 FLDDSTCTGSSGNQVNLITQGLRAMDTGLYICKVELMPPPYEGIGNGTQIVIDPEP 145
 QY 121 CPDSD 125
 DB 146 CPDSD 150
 RESULT 9
 AAV75127 ID AAV75127 standard; Protein: 212 AA.
 XX
 AC AAV75127;
 DT 09-APR-2002 (first entry)
 XX
 DE Human CTLA4 receptor mutant #2.
 XX
 KW Human; rheumatic disease; soluble cytotoxic T lymphocyte antigen 4; Ig;
 KW CTLA4; variable (V)-like extracellular domain; CTLA4lg; B7 molecule;
 KW immunoglobulin constant domain; rheumatoid arthritis; autoimmune disease;
 KW immune system disorder; graft-related disease; immunosuppressive; mutant;
 KW immunoproliferative disease; antiinflammatory; mutein; receptor;
 KW oncostatin M.
 XX
 OS Homo sapiens.
 OS Synthetic.
 OS
 FH Key Location/Qualifiers
 FT Peptide 1..26
 FT Protein /label= Oncostatin_M_Signal_peptide
 FT 27..212
 FT /label= Mature_CTLA4_receptor
 FT Misc-difference 55
 FT /note= "Substitution of wild type Ala to any amino acid"
 FT Misc-difference 130
 FT /note= "Substitution of wild type Leu to Glu"
 PN W0200202638-A2.
 XX
 PD 10-JAN-2002.
 XX
 PF 02-JUL-2001; 2001WO-US21204.
 XX
 PR 03-JUL-2000; 2000US-215913P.
 XX
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.

XX Cohen R, Carr S, Hagerty D, Peach RJ, Becker J;
 PI WPI: 2002-148002/19.
 XX
 XX Composition useful for treating rheumatic disease and immune system
 PT disorders e.g. diabetes mellitus, graft-related disease, good pasture's
 PT syndrome, comprises soluble cytotoxic T lymphocyte A4 mutant molecule
 PT
 XX
 XX Claim 8; Page -: 128pp; English.
 XX
 XX The present invention relates to pharmaceutical compositions and
 CC methods for treating rheumatic disease. The composition comprises a
 CC soluble cytotoxic T lymphocyte antigen 4 (CTLA4) mutant molecule that
 CC blocks endogenous B7 molecules from binding their ligands. Soluble
 CC CTLA4 molecules are constructed by fusing variable (V)-like
 CC extracellular domains of CTLA4 to immunoglobulin (Ig) constant domains
 CC resulting in CTLA4Ig. The composition is useful for treating rheumatic
 CC disease especially rheumatoid arthritis, and for alleviating a symptom
 CC associated with a rheumatic disease from joint swelling, pain,
 CC tenderness, and structural damage. The composition can optionally be used
 CC with other pharmaceutical agents for treating immune system disorders
 CC which include autoimmune diseases (e.g. systemic lupus erythematosus,
 CC Addison's disease, diabetes mellitus, multiple sclerosis, Crohn's
 CC disease, ulcerative colitis, Sjogren's syndrome, scleroderma and
 CC sympathetic ophthalmia), graft-related diseases (e.g. graft-versus-host
 CC disease), immunoproliferative diseases (e.g. psoriasis, T cell lymphoma,
 CC Hashimoto's thyroiditis, pernicious anaemia and good pasture's syndrome).
 CC The present sequence represents a mutant of the human CTLA4 receptor.
 CC Note: The present sequence is not given in the patent but is created by
 CC the indexer from the sequence provided in Fig 23 and the information
 CC given in claim 8.
 XX
 XX Sequence 212 AA;
 SQ
 Query Match 98.8%; Score 649; DB 23; Length 212;
 Best Local Similarity 99.2%; Pred. No. 5.4e-58;
 Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 AMHVAQPAVYVLASRGIAFPCEYASPGKTEYEVYVLRQADSOYTEVCATYMGNELT 60
 DB 26 AMHVAQPAVYVLASRGIAFPCEYASPGKTEYEVYVLRQADSOYTEVCATYMGNELT 85
 QY 61 FLDDISICTGTSSGNQVNLITQGLRAMDTGLYICKVELMPPPYEGIGNQIYVIDEP 120
 DB 86 FLDDISICTGTSSGNQVNLITQGLRAMDTGLYICKVELMPPPYEGIGNQIYVIDEP 145
 QY 121 CPDSD 125
 DB 146 CPDSD 150

RESULT 10
 AAU75132
 ID AAU75132 standard; Protein: 212 AA.
 XX
 XX AAU75132;
 DT 09-APR-2002 (first entry)
 XX
 XX Human CTLA4 receptor mutant #7.
 XX
 XX Human: rheumatic disease; soluble cytotoxic T lymphocyte antigen 4; Ig;
 KW CTLA4; variable (V)-like extracellular domain; CTLA4Ig; B7 molecule;
 KW immunoglobulin constant domain; rheumatoid arthritis; autoimmune disease;
 KW immune system disorder; graft-related disease; immunosuppressive; mutant;
 KW immunoproliferative disease; antiinflammatory; mutein; receptor;
 KW oncostatin M.
 XX
 XX Homo sapiens.
 OS Synthetic.
 OS
 XX

PH Key Location/Qualifiers
 FT Peptide 1..26
 FT /label= Oncostatin_M.Signal_peptide
 FT Protein 27..212
 FT /label= Mature_CTLA4_receptor
 FT Misc-difference 55
 FT /note= "Substitution of wild type Ala to Tyr"
 XX
 XX W0200202638-A2.
 XX
 XX 10-JAN-2002.
 XX
 XX 02-JUL-2001; 2001WO-US21204.
 XX
 XX 03-JUL-2000; 2000US-215913P.
 XX
 XX (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX
 XX Cohen R, Carr S, Hagerty D, Peach RJ, Becker J;
 PI WPI: 2002-148002/19.
 XX
 XX Composition useful for treating rheumatic disease and immune system
 PT disorders e.g. diabetes mellitus, graft-related disease, good pasture's
 PT syndrome, comprises soluble cytotoxic T lymphocyte A4 mutant molecule
 PT
 XX
 XX Claim 12; Page -: 128pp; English.
 XX
 XX The present invention relates to pharmaceutical compositions and
 CC methods for treating rheumatic disease. The composition comprises a
 CC soluble cytotoxic T lymphocyte antigen 4 (CTLA4) mutant molecule that
 CC blocks endogenous B7 molecules from binding their ligands. Soluble
 CC CTLA4 molecules are constructed by fusing variable (V)-like
 CC extracellular domains of CTLA4 to immunoglobulin (Ig) constant domains
 CC resulting in CTLA4Ig. The composition is useful for treating rheumatic
 CC disease especially rheumatoid arthritis, and for alleviating a symptom
 CC associated with a rheumatic disease from joint swelling, pain,
 CC tenderness, and structural damage. The composition can optionally be used
 CC with other pharmaceutical agents for treating immune system disorders
 CC which include autoimmune diseases (e.g. systemic lupus erythematosus,
 CC Addison's disease, diabetes mellitus, multiple sclerosis, Crohn's
 CC disease, ulcerative colitis, Sjogren's syndrome, scleroderma and
 CC sympathetic ophthalmia), graft-related diseases (e.g. graft-versus-host
 CC disease), immunoproliferative diseases (e.g. psoriasis, T cell lymphoma,
 CC Hashimoto's thyroiditis, pernicious anaemia and good pasture's syndrome).
 CC The present sequence represents a mutant of the human CTLA4 receptor.
 CC Note: The present sequence is not given in the patent but is created by
 CC the indexer from the sequence provided in Fig 23 and the information
 CC given in claim 12.
 XX
 XX Sequence 212 AA;
 SQ
 Query Match 98.8%; Score 649; DB 23; Length 212;
 Best Local Similarity 99.2%; Pred. No. 5.4e-58;
 Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 AMHVAQPAVYVLASRGIAFPCEYASPGKTEYEVYVLRQADSOYTEVCATYMGNELT 60
 DB 26 AMHVAQPAVYVLASRGIAFPCEYASPGKTEYEVYVLRQADSOYTEVCATYMGNELT 85
 QY 61 FLDDISICTGTSSGNQVNLITQGLRAMDTGLYICKVELMPPPYEGIGNQIYVIDEP 120
 DB 86 FLDDISICTGTSSGNQVNLITQGLRAMDTGLYICKVELMPPPYEGIGNQIYVIDEP 145
 QY 121 CPDSD 125
 DB 146 CPDSD 150

RESULT 11
 ABB78103
 ID ABB78103 standard; Protein: 383 AA.

XX ABB78103;
 XX
 XX 05-NOV-2002 (first entry)
 XX
 DE Amino acid sequence of a CTLA4lg mutant, designated L104EA29LIg.
 XX
 KM CTLA4lg; mutant; L104EA29LIg; CTLA4; immunoglobulin; Ig; B7;
 KM immunosuppressive; mixed haematopoietic chimerism; transplanted tissue;
 KM T cell depleted bone marrow cell; T cell costimulatory signal;
 KM haemoglobinopathy; beta-thalassemia; sickle cell disease;
 KM organ rejection.
 XX
 OS Synthetic.
 XX
 PN WO200258729-A2.
 XX
 XX 01-AUG-2002.
 XX
 PF 25-JAN-2002; 2002WO-US03780.
 XX
 PR 26-JAN-2001; 2001US-264528P.
 XX 03-JUL-2001; 2001US-303142P.
 XX
 PA (UYEM-) UNIV EMORY.
 XX
 PI Larsen CP, Pearson TC, Waller EK, Adams AB;
 DR WPI: 2002-619143/66.
 DR N-PSDB; ABO78358.
 XX
 PT Establishing mixed haematopoietic chimerism in subject after
 PT transplantation, by administering T cell depleted bone marrow cells,
 PT alkylating agent, immunosuppressive composition that blocks T cell
 PT costimulatory signals -
 XX
 PS Example 8; Fig 16; 161pp; English.
 XX
 CC The present sequence represents a CTLA4lg mutant, designated L104EA29LIg.
 CC CTLA4lg is a soluble fusion protein, comprising an extracellular domain
 CC of wild type CTLA4 joined to an immunoglobulin (Ig) tail or a portion
 CC thereof which binds a B7 molecule. The present protein has the mutations
 CC A39L and L104E. CTLA4lg and its mutants are examples of immunosuppressive
 CC agents that may be used in the method of the invention. The specification
 CC describes a method of establishing mixed haematopoietic chimerism in
 CC a subject with a transplanted tissue. The method comprises administering
 CC to the subject, T cell depleted bone marrow cells, an alkylating agent
 CC and an immunosuppressive composition that blocks T cell costimulatory
 CC signals in the subject, thus establishing haematopoietic chimerism in the
 CC subject. The method is useful for treating haemoglobinopathy
 CC (e.g. beta-thalassemia or sickle cell disease), in a subject by
 CC establishing haematopoietic chimerism. It is also useful for inhibiting
 CC rejection of an organ or tissue transplanted into the subject.
 XX
 SQ Sequence 383 AA;
 Query Match 98.8%; Score 649; DB 23; Length 383;
 Best Local Similarity 99.2%; Pred. No. 1,2e-57;
 Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 12
 AAU75121
 ID AAU75121 standard; Protein; 383 AA.
 XX
 AC AAU75121;
 XX
 DT 09-APR-2002 (first entry)
 XX
 DE Human soluble CTLA4 mutant protein, L104EA29LIg.
 XX
 KM Human; rheumatic disease; soluble cytotoxic T lymphocyte antigen 4; Ig;
 KM CTLA4; variable (V)-like extracellular domain; CTLA4lg; B7 molecule;
 KM immunoglobulin constant domain; rheumatoid arthritis; autoimmune disease;
 KM immune system disorder; graft-related disease; immunosuppressive; mutant;
 KM immunoproliferative disease; antiinflammatory; mutant; L104EA29LIg.
 XX
 OS Homo sapiens.
 OS
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Peptide 1..26
 FT /label= Signal_peptide
 FT Protein 27..383
 FT /label= Mature_L104EA29LIg_mutant
 FT MISC-difference 55
 FT /note= "Substitution of wild type Ala to Leu"
 FT MISC-difference 130
 FT /note= "Substitution of wild type Leu to Glu"
 XX
 PN WO200202638-A2.
 XX
 PD 10-JAN-2002.
 XX
 PF 02-JUL-2001; 2001WO-US21204.
 XX
 PR 03-JUL-2000; 2000US-215913P.
 XX
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX
 PI Cohen R, Carr S, Hagerly D, Peach RJ, Becker J;
 DR WPI: 2002-148002/19.
 DR N-PSDB; AAS20943.
 XX
 PT Composition useful for treating rheumatic disease and immune system
 PT disorders e.g. diabetes mellitus, graft-related disease, good pasture's
 PT syndrome, comprises soluble cytotoxic T lymphocyte A4 mutant molecule
 PT -
 XX
 XX Claim 9; Fig 20; 128pp; English.
 CC The present invention relates to pharmaceutical compositions and
 CC methods for treating rheumatic disease. The composition comprises a
 CC soluble cytotoxic T lymphocyte antigen 4 (CTLA4) mutant molecule that
 CC blocks endogenous B7 molecules from binding their ligands. Soluble
 CC CTLA4 molecules are constructed by fusing variable (V)-like
 CC extracellular domains of CTLA4 to immunoglobulin (Ig) constant domains
 CC resulting in CTLA4lg. The composition is useful for treating rheumatic
 CC disease especially rheumatoid arthritis, and for alleviating a symptom
 CC associated with a rheumatic disease from joint swelling, pain,
 CC tenderness, and structural damage. The composition can optionally be used
 CC with other pharmaceutical agents for treating immune system disorders
 CC which include autoimmune diseases (e.g. systemic lupus erythematosus,
 CC Addison's disease, diabetes mellitus, multiple sclerosis, Crohn's
 CC disease, ulcerative colitis, Sjogren's syndrome, scleroderma and
 CC sympathetic ophthalmia), graft-related diseases (e.g. graft-versus-host
 CC disease), immunoproliferative diseases (e.g. psoriasis, T cell lymphoma,
 CC Hashimoto's thyroiditis, pernicious anaemia and good pasture's syndrome).
 CC The present sequence represents human soluble CTLA4 mutant protein,
 CC L104EA29LIg.
 XX
 SQ Sequence 383 AA;

Query Match 98.8%; Score 649; DB 23; Length 383;
 Best Local Similarity 99.2%; Pred. No. 1.2e-57;
 Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AMHVAOPAVYVLASSRGIAFVCEYASPGKTEVRVTVLRQADSQVTEVCATYMMGNELT 60
 |||||
 DB 26 AMHVAOPAVYVLASSRGIAFVCEYASPGKTEVRVTVLRQADSQVTEVCATYMMGNELT 85
 |||||

QY 61 FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMPPPYEGIGNGTQIYVIDPEP 120
 |||||
 DB 86 FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMPPPYEGIGNGTQIYVIDPEP 145
 |||||

QY 121 CPDSD 125
 |||||
 DB 146 CPDSD 150

RESULT 13
 ABP56719 standard; Protein; 383 AA.
 XX
 AC ABP56719;
 XX
 DT 27-MAR-2003 (first entry)
 XX
 DE CTLA4 mutant L104EA29LIg protein SEQ ID NO:10.
 XX
 KM CTLA4; mutant; islet cell transplantation rejection inhibition;
 KM cytotoxic T lymphocyte associated antigen-4; antidiabetic; antithyroid;
 KM immunoprotective; neuroprotective; dermatological; antipsoriatic;
 KM diabetes; immune system disease; psoriasis; Graves' disease;
 KM multiple sclerosis; oncostatin.
 XX
 OS Homo sapiens.
 OS Synthetic.

Key Location/Qualifiers
 FT Peptide 1..26
 FT /label= oncostatin_signal_peptide
 FT Protein 27..383
 FT /label= CTLA4_mutant_L104EA29LIg
 FT PN WO200294202-A2.
 PD 28-NOV-2002.
 PF 23-MAY-2002; 2002WO-US16708.
 PR 23-MAY-2001; 2001US-293402P.
 PA (UYEM-) UNIV EMORY.
 PI Larsen CP, Pearson TC, Adams AB;
 XX
 DR WPI; 2003-140318/13.
 DR N-PSDB; AB222586.
 XX
 PT Inhibiting islet cell transplant rejection in a subject, useful for
 PT treating diabetes by administering a cytotoxic T lymphocyte associated
 PT antigen-4 mutant molecule
 XX
 PS Claim 2; Fig 20; 100p; English.
 XX
 CC The present invention describes a method of inhibiting islet cell
 CC transplantation rejection in a subject comprising administering a
 CC cytotoxic T lymphocyte associated antigen-4 (CTLA-4) mutant (soluble)
 CC molecule (I), where the subject is transplanted with islet cells before,
 CC or after administration of (I). (I) has antidiabetic, immunoprotective,
 CC neuroprotective, dermatological, antipsoriatic and antithyroid
 CC activities. (I) can be used for inhibiting islet cell transplant
 CC rejection in a subject e.g. a human, non-human primate (preferably
 CC monkey), rabbit, sheep, rat, dog, cat, pig or mouse. The method is useful
 CC for treating diabetes. (I) is also useful for treating immune system

CC diseases e.g. psoriasis, Graves' disease and multiple sclerosis. The
 CC method provides a novel calcineurin inhibitor/steroid-free
 CC immunosuppressive regimen that provides significant protection from
 CC rejection and prolongs the survival of islet allografts in nonhuman
 CC primates. The agent L104EA29LIg is a potent immunosuppressant, and so
 CC replaces tacrolimus in the Edmonton protocol, thereby eliminating the
 CC unwanted side effects of the calcineurin inhibitor. The present sequence
 CC represents a CTLA4 mutant L104EA29LIg protein, which is used in an
 CC example from the present invention.
 XX
 SQ Sequence 383 AA;

Query Match 98.8%; Score 649; DB 24; Length 383;
 Best Local Similarity 99.2%; Pred. No. 1.2e-57;
 Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AMHVAOPAVYVLASSRGIAFVCEYASPGKTEVRVTVLRQADSQVTEVCATYMMGNELT 60
 |||||
 DB 26 AMHVAOPAVYVLASSRGIAFVCEYASPGKTEVRVTVLRQADSQVTEVCATYMMGNELT 85
 |||||

QY 61 FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMPPPYEGIGNGTQIYVIDPEP 120
 |||||
 DB 86 FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMPPPYEGIGNGTQIYVIDPEP 145
 |||||

QY 121 CPDSD 125
 |||||
 DB 146 CPDSD 150

RESULT 14
 AAU75131 standard; Protein; 212 AA.
 XX
 AC AAU75131;
 XX
 DT 09-APR-2002 (first entry)
 XX
 DE Human CTLA4 receptor mutant #6.
 XX
 KM Human: Rheumatic disease; soluble cytotoxic T lymphocyte antigen 4; Ig;
 KM CTLA4; variable (V)-like extracellular domain; CTLA4Ig; B7 molecule;
 KM immunoglobulin constant domain; rheumatoid arthritis; autoimmune disease;
 KM immune system disorder; graft-related disease; immunosuppressive; mutant;
 KM immunoproliferative disease; antinflammatory; muten; receptor;
 KM oncostatin M.
 XX
 OS Homo sapiens.
 OS Synthetic.

Key Location/Qualifiers
 FT Peptide 1..26
 FT /label= Oncostatin_M_Signal_peptide
 FT Protein 27..212
 FT /label= Mature_CTLA4_receptor
 FT MISC-difference 130
 FT /note= "Substitution of wild type Leu to Glu"
 FT PN WO200202638-A2.
 PD 10-JAN-2002.
 PF 02-JUL-2001; 2001WO-US21204.
 PR 03-JUL-2000; 2000US-215913P.
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 PI Cohen R, Carr S, Hagerly D, Peach RJ, Becker J;
 XX
 DR WPI; 2002-148002/19.
 XX
 PT Composition useful for treating rheumatic disease and immune system
 PT disorders e.g. diabetes mellitus, graft-related disease, good pasture's

PT syndrome, comprises soluble cytotoxic T lymphocyte A4 mutant molecule
 PS Claim 12: Page -; 128pp; English.
 CC The present invention relates to pharmaceutical compositions and
 CC methods for treating rheumatic disease. The composition comprises a
 CC soluble cytotoxic T lymphocyte antigen 4 (CTLA4) mutant molecule that
 CC blocks endogenous B7 molecules from binding their ligands. Soluble
 CC CTLA4 molecules are constructed by fusing variable (V)-like
 CC extracellular domains of CTLA4 to immunoglobulin (Ig) constant domains
 CC resulting in CTLA4Ig. The composition is useful for treating rheumatic
 CC disease especially rheumatoid arthritis, and for alleviating a symptom
 CC associated with a rheumatic disease from joint swelling, pain,
 CC tenderness, and structural damage. The composition can optionally be used
 CC with other pharmaceutical agents for treating immune system disorders
 CC which include autoimmune diseases (e.g. systemic lupus erythematosus,
 CC Addison's disease, diabetes mellitus, multiple sclerosis, Crohn's
 CC disease, ulcerative colitis, Sjogren's syndrome, scleroderma and
 CC sympathetic ophthalmia), graft-related diseases (e.g. graft-versus-host
 CC disease), immunoproliferative diseases (e.g. psoriasis, T cell lymphoma,
 CC Hashimoto's thyroiditis), pernicious anaemia and good pasture's syndrome).
 CC The present sequence represents a mutant of the human CTLA4 receptor.
 CC Note: The present sequence is not given in the patent but is created by
 CC the indexer from the sequence provided in Fig 23 and the information
 CC given in claim 12.
 XX
 XX Sequence 212 AA:
 SQ
 Query Match 98.6%; Score 648; DB 23; Length 212;
 Best Local Similarity 99.2%; Pred. No. 6.9e-58;
 Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 AMHVAOPAVYVLASSRGISAFVCEYASPGKYTEVRYTVLRQADSQVTEVCAATYMGNELT 60
 DB 26 AMHVAOPAVYVLASSRGISAFVCEYASPGKYTEVRYTVLRQADSQVTEVCAATYMGNELT 85
 QY 61 FLDDSICTGTSSGNOVNLTIQGLRAMDTGLYICKVELMPPPYEGIGNGTQIYVIDPEP 120
 DB 86 FLDDSICTGTSSGNOVNLTIQGLRAMDTGLYICKVELMPPPYEGIGNGTQIYVIDPEP 145
 QY 121 CPDSD 125
 DB 146 CPDSD 150

RESULT 15
 ABB78101
 ID ABB78101 standard; Protein; 383 AA.
 XX
 AC ABB78101;
 DT 05-NOV-2002 (first entry)
 DE Amino acid sequence of a CTLA4Ig mutant, designated L104E1g.
 XX
 XX CTLA4Ig: mutant; L104E1g; CTLA4; immunoglobulin; Ig; B7;
 KM immunosuppressive; mixed haematopoietic chimerism; transplanted tissue;
 KM T cell depleted bone marrow cell; T cell costimulatory signal;
 KM haemoglobinopathy; beta-thalassemia; sickle cell disease;
 KM organ rejection.
 XX
 OS Synthetic.
 XX
 PN MO200258729-A2.
 XX
 PD 01-AUG-2002.
 XX
 PF 25-JAN-2002; 2002MO-US03780.
 XX
 PR 26-JAN-2001; 2001US-264528P.
 PR 05-JUL-2000; 2001US-303142P.
 XX

PA (UYEM-) UNIV EMORY.
 XX
 PI Larsen CP, Pearson TC, Waller EK, Adams AB;
 XX
 DR WPI; 2002-619143/66.
 XX
 DR N-PSDB; AB078356.
 PT Establishing mixed haematopoietic chimerism in subject after
 PT transplantation, by administering T cell depleted bone marrow cells,
 PT alkylating agent, immunosuppressive composition that blocks T cell
 PT costimulatory signals -
 XX
 PS Example 8; Fig 14; 161pp; English.
 XX
 CC The present sequence represents a CTLA4Ig mutant, designated L104E1g.
 CC CTLA4Ig is a soluble fusion protein, comprising an extracellular domain
 CC of wild type CTLA4 joined to an immunoglobulin (Ig) tail or a portion
 CC thereof which binds a B7 molecule. The present protein has the mutation
 CC L104E. CTLA4Ig and its mutants are examples of immunosuppressive agents
 CC that may be used in the method of the invention. The specification
 CC describes a method of establishing mixed haematopoietic chimerism in
 CC a subject with a transplanted tissue. The method comprises administering
 CC to the subject, T cell depleted bone marrow cells, an alkylating agent
 CC and an immunosuppressive composition that blocks T cell costimulatory
 CC signals in the subject, thus establishing haematopoietic chimerism in the
 CC subject. The method is useful for treating haemoglobinopathy
 CC (e.g. beta-thalassemia or sickle cell disease), in a subject by
 CC establishing haematopoietic chimerism. It is also useful for inhibiting
 CC rejection of an organ or tissue transplanted into the subject.
 XX
 XX Sequence 383 AA:
 SQ
 Query Match 98.6%; Score 648; DB 23; Length 383;
 Best Local Similarity 99.2%; Pred. No. 1.3e-57;
 Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 AMHVAOPAVYVLASSRGISAFVCEYASPGKYTEVRYTVLRQADSQVTEVCAATYMGNELT 60
 DB 26 AMHVAOPAVYVLASSRGISAFVCEYASPGKYTEVRYTVLRQADSQVTEVCAATYMGNELT 85
 QY 61 FLDDSICTGTSSGNOVNLTIQGLRAMDTGLYICKVELMPPPYEGIGNGTQIYVIDPEP 120
 DB 86 FLDDSICTGTSSGNOVNLTIQGLRAMDTGLYICKVELMPPPYEGIGNGTQIYVIDPEP 145
 QY 121 CPDSD 125
 DB 146 CPDSD 150

Search completed: August 23, 2003, 16:54:53
 Job time : 61.5 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 23, 2003, 16:57:06 ; Search time 36 Seconds

(without alignments)
458,200 Million cell updates/sec

Title: US-09-865-321a-4_COPY_26_150
Perfect score: 657
Sequence: 1 AMHVAPAVYVLAASSRGIASF.....GIGNGTQIYIDPECPDSD 125

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 497079 seqs, 131961718 residues

Total number of hits satisfying chosen parameters: 497079

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/ptodata/1/pubppa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubppa/PCF_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubppa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubppa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubppa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubppa/PCFUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubppa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubppa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubppa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubppa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubppa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubppa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubppa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubppa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubppa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/1/pubppa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	657	100.0	383	10	US-09-865-321-4 Sequence 4, Appl1
2	657	100.0	383	11	US-09-898-195A-9 Sequence 9, Appl1
3	657	100.0	383	15	US-10-057-288-4 Sequence 4, Appl1
4	657	100.0	383	15	US-10-155-514-6 Sequence 6, Appl1
5	652	99.2	383	11	US-09-898-195A-15 Sequence 15, Appl1
6	652	99.2	383	15	US-10-057-288-10 Sequence 10, Appl1
7	652	99.2	383	15	US-10-155-514-14 Sequence 14, Appl1
8	649	98.8	383	11	US-09-898-195A-11 Sequence 11, Appl1
9	649	98.8	383	15	US-10-057-288-6 Sequence 6, Appl1
10	649	98.8	383	15	US-10-155-514-10 Sequence 10, Appl1
11	648	98.6	383	11	US-09-865-321-6 Sequence 6, Appl1
12	648	98.6	383	11	US-09-898-195A-7 Sequence 7, Appl1
13	648	98.6	383	11	US-09-898-195A-13 Sequence 13, Appl1
14	648	98.6	383	15	US-10-057-288-2 Sequence 2, Appl1
15	648	98.6	383	15	US-10-057-288-8 Sequence 8, Appl1

16	648	98.6	383	15	US-10-155-514-8	Sequence 8, Appl1
17	648	98.6	383	15	US-10-155-514-12	Sequence 12, Appl1
18	640	97.4	151	15	US-10-207-655-309	Sequence 309, App
19	640	97.4	212	11	US-09-898-195A-17	Sequence 17, Appl1
20	640	97.4	212	15	US-10-057-288-12	Sequence 12, Appl1
21	640	97.4	212	15	US-10-155-514-2	Sequence 2, Appl1
22	640	97.4	374	14	US-10-027-075-26	Sequence 26, Appl1
23	640	97.4	374	14	US-10-027-075-28	Sequence 28, Appl1
24	640	97.4	377	15	US-10-027-075-24	Sequence 24, Appl1
25	640	97.4	382	15	US-10-207-655-307	Sequence 307, App
26	640	97.4	382	15	US-10-207-655-316	Sequence 316, App
27	640	97.4	383	10	US-09-865-321-8	Sequence 8, Appl1
28	640	97.4	383	11	US-09-898-195A-19	Sequence 19, Appl1
29	640	97.4	383	15	US-10-057-288-14	Sequence 14, Appl1
30	640	97.4	383	15	US-10-155-514-4	Sequence 4, Appl1
31	640	97.4	383	15	US-10-155-514-16	Sequence 16, Appl1
32	640	97.4	399	15	US-10-207-655-320	Sequence 320, App
33	640	97.4	403	15	US-10-207-655-318	Sequence 318, App
34	635	96.7	223	11	US-09-835-297-2	Sequence 2, Appl1
35	635	96.7	223	15	US-10-211-207-3	Sequence 3, Appl1
36	634	96.5	168	10	US-09-845-899A-7	Sequence 7, Appl1
37	634	96.5	223	10	US-09-989-545-21	Sequence 21, Appl1
38	634	96.5	223	15	US-10-225-519-8	Sequence 8, Appl1
39	634	96.5	223	15	US-10-207-655-101	Sequence 101, App
40	630	95.9	260	15	US-10-225-519-4	Sequence 4, Appl1
41	628	95.6	124	15	US-10-207-655-314	Sequence 314, App
42	627	95.4	167	11	US-09-014-761-1	Sequence 1, Appl1
43	627	95.4	223	14	US-10-107-828-26	Sequence 26, Appl1
44	627	95.4	223	14	US-10-107-907-26	Sequence 26, Appl1
45	627	95.4	223	14	US-10-107-868-26	Sequence 26, Appl1

ALIGNMENTS

RESULT 1
US-09-865-321-4
Sequence 4, Application US/09865321
Publication No. US20020182211A1
GENERAL INFORMATION:
APPLICANT: Peach, Robert J.
APPLICANT: Naemura, Joseph R.
APPLICANT: Insley, Peter S.
APPLICANT: Bajorath, Jürgen
TITLE OF INVENTION: SOLUBLE CITRA4 MUTANT MOLECULES AND USES THEREOF
FILE REFERENCE: DB28VP/30436.57US01
CURRENT APPLICATION NUMBER: US/09/865,321
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: 60/287,576
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/214,065
PRIOR FILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 383
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: L104EA29Y1g
US-09-865-321-4

Query Match 100.0%; Score 657; DB 10; Length 383;
Best Local Similarity 100.0%; Pred. No. 2.8e-61;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMHVAPAVYVLAASSRGIASFVCEYASPGKTEYRVTVLRQADSQVTEVCATYMGNEILT 60
DB 26 AMHVAPAVYVLAASSRGIASFVCEYASPGKTEYRVTVLRQADSQVTEVCATYMGNEILT 85
QY 61 FLDSDICTGTSSGNVNLTIQGLRAMDTGLYICKVELAMPPPYEIGNGTQIYIDPEP 120
DB 86 FLDSDICTGTSSGNVNLTIQGLRAMDTGLYICKVELAMPPPYEIGNGTQIYIDPEP 145


```

: TITLE OF INVENTION: METHODS FOR TREATING RHEUMATIC DISEASES USING A SOLUBLE
: FILE OF INVENTION: CT1A4 MOLECULE
: FILE REFERENCE: D0030NP/30436.55USU1
: CURRENT APPLICATION NUMBER: US/09/898,195A
: PRIOR FILING DATE: 2002-04-15
: PRIOR APPLICATION NUMBER: 60/215,913
: NUMBER OF SEQ ID NOS: 19
: SOFTWARE: Patentln Ver. 2.1
: SEQ ID NO 15
: LENGTH: 383
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: L104EA29WTg
US-09-898-195A-15

Query Match          99.2%; Score 652; DB 11; Length 383;
Best Local Similarity 99.2%; Pred. No. 9.3e-61;
Matches 124; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMHYAOPAVYLVASSRGISAFCEYASPGKTEVRVTVLRADSOVTEVCATYMMGNELT 60
    |||||||
DB 26 AMHYAOPAVYLVASSRGISAFCEYASPGKTEVRVTVLRADSOVTEVCATYMMGNELT 85
    |||||||

QY 61 FLDDISCTGSSGNQVNLITIGLRAMDGLYICKVELMPPPYEGIGNGTQIYVIDEP 120
    |||||||
DB 86 FLDDISCTGSSGNQVNLITIGLRAMDGLYICKVELMPPPYEGIGNGTQIYVIDEP 145
    |||||||

QY 121 CPDSD 125
    |||||
DB 146 CPDSD 150

RESULT 6
US-10-057-288-10
: Sequence 10, Application US/10057288
: Publication No. US20030007968A1
: GENERAL INFORMATION:
: APPLICANT: Larsen, Christian P.
: APPLICANT: Pearson, Thomas C.
: APPLICANT: Waller, Edmund K.
: APPLICANT: Adams, Andrew B.
: TITLE OF INVENTION: METHODS OF INDUCING ORGAN TRANSPLANT TOLERANCE AND
: TITLE OF INVENTION: CORRECTING HEMOGLOBINOPATHIES
: FILE REFERENCE: D0136NP/30436.58USU1
: CURRENT APPLICATION NUMBER: US/10/057,288
: PRIOR FILING DATE: 2002-01-25
: PRIOR APPLICATION NUMBER: 60/264,528
: PRIOR FILING DATE: 2001-01-26
: PRIOR APPLICATION NUMBER: 60/303,142
: PRIOR FILING DATE: 2001-07-05
: NUMBER OF SEQ ID NOS: 20
: SOFTWARE: Patentln Ver. 2.1
: SEQ ID NO 10
: LENGTH: 383
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: L104EA29WTg
US-10-057-288-10

Query Match          99.2%; Score 652; DB 15; Length 383;
Best Local Similarity 99.2%; Pred. No. 9.3e-61;
Matches 124; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMHYAOPAVYLVASSRGISAFCEYASPGKTEVRVTVLRADSOVTEVCATYMMGNELT 60
    |||||||
DB 26 AMHYAOPAVYLVASSRGISAFCEYASPGKTEVRVTVLRADSOVTEVCATYMMGNELT 85
    |||||||

QY 61 FLDDISCTGSSGNQVNLITIGLRAMDGLYICKVELMPPPYEGIGNGTQIYVIDEP 120
    |||||||
DB 86 FLDDISCTGSSGNQVNLITIGLRAMDGLYICKVELMPPPYEGIGNGTQIYVIDEP 145
    |||||||

QY 121 CPDSD 125
    |||||
DB 146 CPDSD 150

RESULT 7
US-10-155-514-14
: Sequence 14, Application US/10155514
: Publication No. US20030022836A1
: GENERAL INFORMATION:
: APPLICANT: Larsen, Christian P.
: APPLICANT: Pearson, Thomas C.
: APPLICANT: Adams, Andrew B.
: TITLE OF INVENTION: METHODS FOR PROTECTING ALLOGENEIC ISLET TRANSPLANT USING SOLU
: FILE OF INVENTION: MUTANT MOLECULES
: FILE REFERENCE: D0173NP / 30436.62USU1
: CURRENT APPLICATION NUMBER: US/10/155,514
: PRIOR FILING DATE: 2002-09-06
: PRIOR APPLICATION NUMBER: 60/293,402
: PRIOR FILING DATE: 2001-05-23
: NUMBER OF SEQ ID NOS: 18
: SOFTWARE: Patentln version 3.1
: SEQ ID NO 14
: LENGTH: 383
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: L104EA29WTg sequence
US-10-155-514-14

Query Match          99.2%; Score 652; DB 15; Length 383;
Best Local Similarity 99.2%; Pred. No. 9.3e-61;
Matches 124; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMHYAOPAVYLVASSRGISAFCEYASPGKTEVRVTVLRADSOVTEVCATYMMGNELT 60
    |||||||
DB 26 AMHYAOPAVYLVASSRGISAFCEYASPGKTEVRVTVLRADSOVTEVCATYMMGNELT 85
    |||||||

QY 61 FLDDISCTGSSGNQVNLITIGLRAMDGLYICKVELMPPPYEGIGNGTQIYVIDEP 120
    |||||||
DB 86 FLDDISCTGSSGNQVNLITIGLRAMDGLYICKVELMPPPYEGIGNGTQIYVIDEP 145
    |||||||

QY 121 CPDSD 125
    |||||
DB 146 CPDSD 150

RESULT 8
US-09-898-195A-11
: Sequence 11, Application US/09898195A
: Publication No. US20030083246A1
: GENERAL INFORMATION:
: APPLICANT: Cohen, Robert
: APPLICANT: Carr, Suzette
: APPLICANT: Hagerly, David
: APPLICANT: Beach, Robert J
: APPLICANT: Becker, Jean-Claude
: TITLE OF INVENTION: METHODS FOR TREATING RHEUMATIC DISEASES USING A SOLUBLE
: FILE OF INVENTION: CT1A4 MOLECULE
: FILE REFERENCE: D0030NP/30436.55USU1
: CURRENT APPLICATION NUMBER: US/09/898,195A
: PRIOR FILING DATE: 2002-04-15
: PRIOR APPLICATION NUMBER: 60/215,913
: PRIOR FILING DATE: 2000-07-03
: NUMBER OF SEQ ID NOS: 19
: SOFTWARE: Patentln Ver. 2.1
: SEQ ID NO 11
: LENGTH: 383
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
```

```
; OTHER INFORMATION: Description of Artificial Sequence: L104EA29Lig
US-09-898-195A-11
Query Match          98.8%; Score 649; DB 11; Length 383;
Best Local Similarity 99.2%; Pred. No. 1.9e-60;
Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AMHVAQPAVVLASSRGIASFVCEYASPGKYTEVRVTVLRQADSOVTEVCATYMMGNELT 60
    |||||||
DB 26 AMHVAQPAVVLASSRGIASFVCEYASPGKLTEVRVTVLRQADSOVTEVCATYMMGNELT 85
    |||||||

QY 61 FLDDSTCTGSSGNQVNLTIQGLRAMDTGLYICKVELMPPPYEGIGNGTQIYVIDPEP 120
    |||||||
DB 86 FLDDSTCTGSSGNQVNLTIQGLRAMDTGLYICKVELMPPPYEGIGNGTQIYVIDPEP 145
    |||||||

QY 121 CPDSD 125
    |||||
DB 146 CPDSD 150

RESULT 9
US-10-057-288-6
; Sequence 6, Application US/10057288
; Publication No. US20030007968A1
; GENERAL INFORMATION:
; APPLICANT: Larsen, Christian P.
; APPLICANT: Pearson, Thomas C.
; APPLICANT: Waller, Edmund K.
; APPLICANT: Adams, Andrew B.
; TITLE OF INVENTION: METHODS OF INDUCING ORGAN TRANSPLANT TOLERANCE AND
; FILE REFERENCE: D0136NP/30436.58US01
; CURRENT APPLICATION NUMBER: US/10/057,288
; CURRENT FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: 60/264,528
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/303,142
; PRIOR FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 6
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: L104EA29Lig
US-10-057-288-6

Query Match          98.8%; Score 649; DB 15; Length 383;
Best Local Similarity 99.2%; Pred. No. 1.9e-60;
Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AMHVAQPAVVLASSRGIASFVCEYASPGKYTEVRVTVLRQADSOVTEVCATYMMGNELT 60
    |||||||
DB 26 AMHVAQPAVVLASSRGIASFVCEYASPGKLTEVRVTVLRQADSOVTEVCATYMMGNELT 85
    |||||||

QY 61 FLDDSTCTGSSGNQVNLTIQGLRAMDTGLYICKVELMPPPYEGIGNGTQIYVIDPEP 120
    |||||||
DB 86 FLDDSTCTGSSGNQVNLTIQGLRAMDTGLYICKVELMPPPYEGIGNGTQIYVIDPEP 145
    |||||||

QY 121 CPDSD 125
    |||||
DB 146 CPDSD 150

RESULT 10
US-10-155-514-10
; Sequence 10, Application US/10155514
; Publication No. US20030022836A1
; GENERAL INFORMATION:
; APPLICANT: Larsen, Christian P.
; APPLICANT: Pearson, Thomas C.

; APPLICANT: Adams, Andrew B.
; TITLE OF INVENTION: METHODS FOR PROTECTING ALLOGENEIC ISLET TRANSPLANT USING SOLUB
; FILE REFERENCE: D0173NP / 30436.62US01
; CURRENT APPLICATION NUMBER: US/10/155,514
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: 60/293,402
; PRIOR FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 10
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: L104EA29Lig sequence
US-10-155-514-10

Query Match          98.8%; Score 649; DB 15; Length 383;
Best Local Similarity 99.2%; Pred. No. 1.9e-60;
Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AMHVAQPAVVLASSRGIASFVCEYASPGKYTEVRVTVLRQADSOVTEVCATYMMGNELT 60
    |||||||
DB 26 AMHVAQPAVVLASSRGIASFVCEYASPGKLTEVRVTVLRQADSOVTEVCATYMMGNELT 85
    |||||||

QY 61 FLDDSTCTGSSGNQVNLTIQGLRAMDTGLYICKVELMPPPYEGIGNGTQIYVIDPEP 120
    |||||||
DB 86 FLDDSTCTGSSGNQVNLTIQGLRAMDTGLYICKVELMPPPYEGIGNGTQIYVIDPEP 145
    |||||||

QY 121 CPDSD 125
    |||||
DB 146 CPDSD 150

RESULT 11
US-09-865-321-6
; Sequence 6, Application US/09865321
; Publication No. US20020182211A1
; GENERAL INFORMATION:
; APPLICANT: Peach, Robert J.
; APPLICANT: Naemura, Joseph R.
; APPLICANT: Linsley, Peter S.
; APPLICANT: Bajorath, Jurgen
; TITLE OF INVENTION: SOLUBLE CTLA4 MUTANT MOLECULES AND USES THEREOF
; FILE REFERENCE: DB28NP/30436.57US01
; CURRENT APPLICATION NUMBER: US/09/865,321
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/287,576
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/214,065
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 6
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: L104E1g
US-09-865-321-6

Query Match          98.6%; Score 648; DB 10; Length 383;
Best Local Similarity 99.2%; Pred. No. 2.5e-60;
Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AMHVAQPAVVLASSRGIASFVCEYASPGKYTEVRVTVLRQADSOVTEVCATYMMGNELT 60
    |||||||
DB 26 AMHVAQPAVVLASSRGIASFVCEYASPGKYTEVRVTVLRQADSOVTEVCATYMMGNELT 85
    |||||||

QY 61 FLDDSTCTGSSGNQVNLTIQGLRAMDTGLYICKVELMPPPYEGIGNGTQIYVIDPEP 120
    |||||||
DB 86 FLDDSTCTGSSGNQVNLTIQGLRAMDTGLYICKVELMPPPYEGIGNGTQIYVIDPEP 145
    |||||||
```



```

1  APPLICANT: Adams, Andrew B.
2  TITLE OF INVENTION: METHODS OF INDUCING ORGAN TRANSPLANT TOLERANCE AND
3  TITLE OF INVENTION: CORRECTING HEMOGLOBINOPATHIES
4  FILE REFERENCE: D0136NP/30436.58USU1
5  CURRENT APPLICATION NUMBER: US/10/057, 288
6  CURRENT FILING DATE: 2002-01-25
7  PRIOR APPLICATION NUMBER: 60/264, 528
8  PRIOR FILING DATE: 2001-01-26
9  PRIOR APPLICATION NUMBER: 60/303, 142
10 PRIOR FILING DATE: 2001-07-05
11 NUMBER OF SEQ ID NOS: 20
12 SOFTWARE: PatentIn Ver. 2.1
13 SEQ ID NO 8
14     LENGTH: 383
15     TYPE: PRT
16 ORGANISM: Artificial Sequence
17 FEATURE:
18 OTHER INFORMATION: Description of Artificial Sequence: L104EA29T1g
19 US-10-057-288-8

```

Query Match	98.6%	Score 648;	DB 15;	Length 383;
Best Local Similarity	99.2%;	Pred. No. 2.5e-60;		
Matches 124;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;

[illegible]

Search completed: August 23, 2003, 17:09:43
Job time : 37 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 23, 2003, 16:52:21 ; Search time 20.5 Seconds

(Without alignments)
257,993 Million cell updates/sec

Title: US-09-865-321a-4_COPY_26_150

Perfect score: 1 AMHVAQPAVVLASSRGIA SF.....GICNGIQIYIDPEPCDSD 125

Sequence: 657

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*

2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*

3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*

4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*

5: /cgn2_6/ptodata/1/1aa/PCFUS.COMB.pep.*

6: /cgn2_6/ptodata/1/1aa/Backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	640	97.4	187 1 US-08-067-684-14	Sequence 14, Appl
2	640	97.4	187 1 US-08-008-898-14	Sequence 14, Appl
3	640	97.4	187 2 US-08-459-818-14	Sequence 14, Appl
4	640	97.4	187 2 US-08-889-666-14	Sequence 14, Appl
5	640	97.4	187 2 US-08-465-078-14	Sequence 14, Appl
6	640	97.4	187 2 US-08-725-776-14	Sequence 14, Appl
7	640	97.4	187 2 US-08-488-062-14	Sequence 14, Appl
8	640	97.4	187 3 US-08-228-208A-14	Sequence 14, Appl
9	640	97.4	187 3 US-08-228-208A-17	Sequence 17, Appl
10	640	97.4	187 4 US-09-227-595-26	Sequence 26, Appl
11	640	97.4	187 4 US-09-227-595-28	Sequence 26, Appl
12	640	97.4	187 4 US-09-227-595-24	Sequence 26, Appl
13	637	97.0	187 5 PCT-US95-06726-36	Sequence 24, Appl
14	631	96.0	124 3 US-08-630-172-4	Sequence 36, Appl
15	631	96.0	124 3 US-09-375-419-4	Sequence 4, Appl
16	631	96.0	357 3 US-08-630-172-20	Sequence 20, Appl
17	631	96.0	357 3 US-09-375-419-20	Sequence 20, Appl
18	617.5	94.0	253 2 US-08-459-818-20	Sequence 20, Appl
19	617.5	94.0	253 2 US-08-889-666-20	Sequence 20, Appl
20	617.5	94.0	253 2 US-08-465-078-20	Sequence 20, Appl
21	617.5	94.0	253 2 US-08-725-776-20	Sequence 20, Appl
22	617.5	94.0	253 2 US-08-488-062-20	Sequence 20, Appl
23	617.5	94.0	502 2 US-08-459-818-19	Sequence 19, Appl
24	617.5	94.0	502 2 US-08-889-666-19	Sequence 19, Appl
25	617.5	94.0	502 2 US-08-465-078-19	Sequence 19, Appl
26	617.5	94.0	502 2 US-08-725-776-19	Sequence 19, Appl
27	617.5	94.0	502 2 US-08-488-062-19	Sequence 19, Appl

28	602	91.6	234 1 US-08-505-058-1	Sequence 1, Appl
29	602	91.6	234 2 US-08-459-818-21	Sequence 21, Appl
30	602	91.6	234 2 US-08-889-666-21	Sequence 21, Appl
31	602	91.6	234 2 US-08-465-078-21	Sequence 21, Appl
32	602	91.6	234 2 US-08-725-776-21	Sequence 21, Appl
33	602	91.6	234 2 US-08-488-062-21	Sequence 21, Appl
34	584	88.9	137 3 US-08-804-180C-2	Sequence 2, Appl
35	570	86.8	238 4 US-09-227-595-30	Sequence 30, Appl
36	570	86.8	238 4 US-09-227-595-32	Sequence 32, Appl
37	550	83.7	109 4 US-09-460-384-34	Sequence 34, Appl
38	541	82.3	223 4 US-09-303-040-10	Sequence 10, Appl
39	434	66.1	223 3 US-08-228-208A-18	Sequence 18, Appl
40	420	63.9	174 3 US-08-804-180C-4	Sequence 4, Appl
41	404	61.5	234 1 US-08-505-058-2	Sequence 2, Appl
42	404	61.5	234 2 US-08-459-818-22	Sequence 22, Appl
43	404	61.5	234 2 US-08-889-666-22	Sequence 22, Appl
44	404	61.5	234 2 US-08-465-078-22	Sequence 22, Appl
45	404	61.5	234 2 US-08-725-776-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1
US-08-067-684-14
Sequence 14, Application US/08067684
Patent No. 5434131
GENERAL INFORMATION:
APPLICANT: Linsley, Peter S.
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Damle, Nitin K.
APPLICANT: Brady, William
TITLE OF INVENTION: CTLA4 RECEPTOR AND METHODS FOR ITS USE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESS: Sheldon & Mak
STREET: 225 South Lake Avenue, Suite 900
CITY: Pasadena
STATE: California
COUNTRY: U.S.A.
ZIP: 91101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/067,684
FILING DATE: 26-MAY-1993
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B.
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 7848-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310/312-0900
TELEFAX: 310/479-8340
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 187 amino acids
TYPE: amino acid
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
US-08-067-684-14
Query Match 97.4% Score 640; DB 1; Length 187;
Best Local Similarity 98.4% Pred. No. 6e-65;
Matches 123; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
1 AMHVAQPAVVLASSRGIA SFCEYASPGKTEVTVLRADSOVTECATYMGNELT 60
|||||

Db 1 AMHVAOPAVYLAASSRGIAFVCEYASPGKATEVRVTVLRQADSQVTEVCAATYMMGNELT 60
QY 61 FLDSDICGTSSGNOVNLTIOGLRAMDTGLYICKVELMPPRYEGISGNGTOIYYIDPEP 120
Db 61 FLDSDICGTSSGNOVNLTIOGLRAMDTGLYICKVELMPPRYEGISGNGTOIYYIDPEP 120
QY 121 CPDSD 125
Db 121 CPDSD 125

RESULT 2

US-08-008-898-14
; Sequence 14, Application US/08008898
; Patent No. 5770197
; GENERAL INFORMATION:
; APPLICANT: Linsley, Peter S
; APPLICANT: Ledbetter, Jeffrey A
; APPLICANT: Damle, Nitin K
; APPLICANT: Brady, William
; TITLE OF INVENTION: CTLA4 RECEPTOR AND METHODS FOR ITS USE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 201 South Lake Avenue, Suite 800
; CITY: Pasadena
; STATE: California
; COUNTRY: United States
; ZIP: 91101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/008,898
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/723,617
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandel, Saralynn
; REGISTRATION NUMBER: 31,853
; REFERENCE/DOCKET NUMBER: 7848
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (818) 796-4000
; TELEFAX: (818) 795-6321
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 187 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-008-898-14

Query Match 97.4%; Score 640; DB 1; Length 187;
Best Local Similarity 98.4%; Pred. No. 6e-65;
Matches 123; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AMHVAOPAVYLAASSRGIAFVCEYASPGKATEVRVTVLRQADSQVTEVCAATYMMGNELT 60
Db 1 AMHVAOPAVYLAASSRGIAFVCEYASPGKATEVRVTVLRQADSQVTEVCAATYMMGNELT 60
QY 61 FLDSDICGTSSGNOVNLTIOGLRAMDTGLYICKVELMPPRYEGISGNGTOIYYIDPEP 120
Db 61 FLDSDICGTSSGNOVNLTIOGLRAMDTGLYICKVELMPPRYEGISGNGTOIYYIDPEP 120
QY 121 CPDSD 125
Db 121 CPDSD 125

RESULT 3

US-08-459-818-14
; Sequence 14, Application US/08459818
; Patent No. 5851795
; GENERAL INFORMATION:
; APPLICANT: Linsley, Peter S.
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Damle, Nitin K.
; APPLICANT: Brady, William
; TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 1150 Santa Monica Blvd., Suite 400
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Fastseq 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,818
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Adriano, Sarah B.
; REGISTRATION NUMBER: 34,470
; REFERENCE/DOCKET NUMBER: 30436.35US02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-445-1140
; TELEFAX: 310-445-9031
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 187 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-459-818-14

Query Match 97.4%; Score 640; DB 2; Length 187;
Best Local Similarity 98.4%; Pred. No. 6e-65;
Matches 123; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AMHVAOPAVYLAASSRGIAFVCEYASPGKATEVRVTVLRQADSQVTEVCAATYMMGNELT 60
Db 1 AMHVAOPAVYLAASSRGIAFVCEYASPGKATEVRVTVLRQADSQVTEVCAATYMMGNELT 60
QY 61 FLDSDICGTSSGNOVNLTIOGLRAMDTGLYICKVELMPPRYEGISGNGTOIYYIDPEP 120
Db 61 FLDSDICGTSSGNOVNLTIOGLRAMDTGLYICKVELMPPRYEGISGNGTOIYYIDPEP 120
QY 121 CPDSD 125
Db 121 CPDSD 125

RESULT 4

US-08-889-666-14
; Sequence 14, Application US/08889666
; Patent No. 5885579
; GENERAL INFORMATION:
; APPLICANT: Linsley, Peter S.
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Damle, Nitin K.
; APPLICANT: Brady, William
; APPLICANT: Kiener, Peter A.
; TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 23, 2003, 16:50:56 ; Search time 24.5 Seconds

(without alignments)
490.657 Million cell updates/sec

Title: US-09-865-321a-8_COPY_26_150

Sequence: 1 AMHYAOPAVVIASSRGIA SF.....GIGNGTQIYVIDPEPCDSD 125

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 segs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	647	99.1	223	2	T09536
2	644	98.6	186	2	S08614
3	561	85.9	223	2	I46696
4	458	70.1	223	2	A29063
5	150	23.0	221	2	S25168
6	139	21.3	173	2	I46197
7	127.5	19.5	220	1	RWHU28
8	121	18.5	221	2	I46689
9	121	17.5	218	2	A43523
10	114	15.4	218	2	S24413
11	100.5	15.4	120	2	S46370
12	99	15.2	124	2	S40336
13	95.5	14.6	108	2	S36277
14	95.5	14.6	132	2	S38646
15	94.5	14.5	140	2	PL0013
16	94	14.4	125	2	S40353
17	93.5	14.3	128	2	S46372
18	93	14.2	108	2	S30521
19	92.5	14.2	117	2	S46371
20	92.5	14.2	117	2	S46371
21	91	13.9	120	2	A21177
22	90.5	13.9	132	2	S40334
23	90	13.8	111	2	S36281
24	89.5	13.7	105	2	S26338
25	89	13.6	111	2	S38497
26	89	13.6	112	2	H26317
27	88.5	13.6	108	2	S36279
28	88	13.5	111	1	L2HUTG
29	88	13.5	111	1	L2HUTR

30	87.5	13.4	123	2	S40378	Ig kappa chain - h
31	87	13.3	92	2	S37504	Ig kappa chain V r
32	87	13.3	104	2	JC6076	anti-D-dimer monoc
33	87	13.3	108	2	S34007	Ig kappa chain V r
34	87	13.3	112	2	PL0274	Ig kappa chain V r
35	86.5	13.2	107	2	S12954	Ig kappa chain V r
36	86	13.2	92	2	S37516	Ig kappa chain V r
37	86	13.2	111	2	S19671	Ig kappa chain V
38	86	13.2	129	2	S40369	Ig kappa chain - h
39	85.5	13.1	124	2	S40338	Ig kappa chain V r
40	85.5	13.1	125	2	S40350	Ig kappa chain - h
41	85.5	13.1	212	2	S70431	Ig kappa chain - h
42	85.5	13.1	235	2	S14675	Ig kappa chain - h
43	84.5	12.9	108	2	G44151	Ig kappa chain V r
44	84.5	12.9	110	2	S60591	Ig light chain var
45	84.5	12.9	111	2	PM0537	Ig kappa chain V r

ALIGNMENTS

RESULT 1
T09536
cytotoxic T-lymphocyte protein 4 - human
C:Species: Homo sapiens (man)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C:Accession: T09536
R:Harper, K.; Balzano, C.; Rouvler, E.; Mattei, M.G.; Luciani, M.F.; Golstein, P.
J. Immunol. 147, 1037-1044, 1991
A:Title: CTLA-4 and CD28 activated lymphocyte molecules are closely related in both n
A:Reference number: I49584; MUID:91318145; PMID:1713603
A:Accession: T09536
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-223 <HAR>
A:Cross-references: EMBL:LI5006; NID:9291928; PIDN:AA859385.1; PID:9291929
C:Gene: CTLA4
A:Map position: 2q33
C:Superfamily: T-cell surface glycoprotein CD28; immunoglobulin homology
C:Keywords: T-cell; transmembrane protein

Query Match 99.1% Score 647; DB 2; Length 223;
Best Local Similarity 99.2% Pred. No. 3e-57; 1; Indels 0; Gaps 0;
Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 AMHYAOPAVVIASSRGIA SFCEYASPKATEVRYVLRQDSQVTEVCATYMGNELT 60
|||||
DB 37 AMHYAOPAVVIASSRGIA SFCEYASPKATEVRYVLRQDSQVTEVCATYMGNELT 96
OY 61 FLDSICTGSSGNQVNLITGLRMDTGIXCKVELMYPPYYLGIGNGTQIYVIDPEP 120
|||||
DB 97 FLDSICTGSSGNQVNLITGLRMDTGIXCKVELMYPPYYLGIGNGTQIYVIDPEP 156
OY 121 CPDSD 125
|||||
DB 157 CPDSD 161

RESULT 2
S08614
cytotoxic T-lymphocyte protein 4 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 11-Jan-2000
C:Accession: S08614
R:Darlavach, P.; Mattei, M.G.; Golstein, P.; Letfranc, M.P.
Eur. J. Immunol. 18, 1901-1905, 1988
A:Title: Human Ig superfamily CTLA-4 gene: chromosomal localization and identity of p
A:Reference number: S08614; MUID:89120925; PMID:3220103
A:Accession: S08614
A:Molecule type: DNA
A:Residues: 1-186 <DAR>
A:Cross-references: EMBL:X15070; NID:930283; PID:9825649

C:Genetics:
 A:Gene: GDB:CTLA4
 A:Cross-references: GDB:119818; OMIM:123890
 A:Map position: 2q33-2q33
 A:Introns: 116/1; 152/3
 C:Superfamily: T-cell surface glycoprotein CD28; immunoglobulin homology
 C:Keywords: transmembrane protein
 F:115-150/Domain: intracellular #status predicted <TM>
 F:151-186/Domain: intracellular #status predicted <INT>
 F:21-92/Disulfide bonds: #status predicted

Query Match
 Best Local Similarity: 98.6%; Score 644; DB 2; Length 186;
 Matches 123; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 MHVAQPAVAVLASSRGISFVCEYASPGKATEVRVTVLRQADSOVTEVCATYMGNELTF 61
 D 1 MHVAQPAVAVLASSRGISFVCEYASPGKATEVRVTVLRQADSOVTEVCATYMGNELTF 60
 QY 62 LDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMPPPYVYLGISNGTOIYVIDEPC 121
 D 61 LDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMPPPYVYLGISNGTOIYVIDEPC 120
 QY 122 PDSD 125
 D 121 PDSD 124

RESULT 3
 146696
 CTLA-4 precursor - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 05-Nov-1999
 C:Accession: 146696
 R:Isono, T.; Seto, A.
 Immunogenetics 42, 217-220, 1995
 A:Title: Cloning and sequencing of the rabbit gene encoding T-cell costimulatory molecule
 A:Reference number: 146689; MUID:95369849; PMID:7642234
 A:Accession: 146696
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-223 <ISO>
 A:Cross-references: GB:D49844; NID:9755100; PIDN:BAA08644.1; PID:9755101
 C:Superfamily: T-cell surface glycoprotein CD28; immunoglobulin homology

Query Match
 Best Local Similarity: 85.9%; Score 561; DB 2; Length 223;
 Matches 105; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

QY 1 AMHVAQPAVAVLASSRGISFVCEYASPGKATEVRVTVLRQADSOVTEVCATYMGNELTF 60
 D 37 AMHVAQPAVAVLASSRGISFVCEYASPGKATEVRVTVLRQADSOVTEVCATYMGNELTF 96
 QY 61 FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMPPPYVYLGISNGTOIYVIDEPC 120
 D 97 FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMPPPYVYLGISNGTOIYVIDEPC 156
 QY 121 CPDSD 125
 D 157 CPDSD 161

RESULT 4
 A29063
 cytotoxic T-lymphocyte protein 4 - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 05-Nov-1999
 C:Accession: A29063; I49622
 R:Brune, J.F.; Denicourt, F.; Luciani, M.F.; Roux-Dosseco, M.; Suzan, M.; Mattel, M.G.;
 Nature 328, 267-270, 1987
 A:Title: A new member of the immunoglobulin superfamily--CTLA-4.
 A:Reference number: A29063; MUID:87258259; PMID:3496540
 C:Accession: A29063

A:Molecule type: mRNA
 A:Residues: 1-223 <BRD>
 A:Cross-references: GB:X05719; NID:g50592; PIDN:CAA29191.1; PID:g50593
 A:Harper, K.; Balzano, C.; Rouvier, E.; Mattel, M.G.; Luciani, M.F.; Golstein, P.
 J. Immunol. 147, 1037-1044, 1991
 A:Title: CTLA-4 and CD28 activated lymphocyte molecules are closely related in both m
 A:Reference number: I49584; MUID:91318145; PMID:1713603
 A:Accession: I49622
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-36 <RES>
 A:Cross-references: GB:M74362; NID:g192833; PIDN:AAA37489.1; PID:g553903
 C:Genetics:
 A:Gene: CtlA-4
 A:Map position: 1, band C
 C:Superfamily: T-cell surface glycoprotein CD28; immunoglobulin homology
 C:Keywords: transmembrane protein

Query Match
 Best Local Similarity: 70.1%; Score 458; DB 2; Length 223;
 Matches 85; Conservative 17; Mismatches 23; Indels 0; Gaps 0;

QY 1 AMHVAQPAVAVLASSRGISFVCEYASPGKATEVRVTVLRQADSOVTEVCATYMGNELTF 60
 D 37 AIGVQPSVAVLASHGVASPECEYSPSHNDEVTVLRQTDOMEVCATFTETKNTVG 96
 QY 61 FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMPPPYVYLGISNGTOIYVIDEPC 120
 D 97 FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMPPPYVYLGISNGTOIYVIDEPC 156
 QY 121 CPDSD 125
 D 157 CPDSD 161

RESULT 5
 525168
 CH78 protein - chicken
 C:Species: Gallus gallus (chicken)
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
 C:Accession: I50619; S25168
 R:Young, J.R.; Davison, T.F.; Tregaskes, C.A.; Renne, M.C.; Vainio, O.
 J. Immunol. 152, 3848-3851, 1994
 A:Title: Monomeric homologue of mammalian CD28 is expressed on chicken T cells.
 A:Reference number: I50619; MUID:94194147; PMID:8144954
 A:Accession: I50619
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-221 <YO2>
 A:Cross-references: EMBL:X67915; NID:g63221; PIDN:CAA48114.1; PID:g63222
 C:Superfamily: T-cell surface glycoprotein CD28; immunoglobulin homology
 C:Keywords: transmembrane protein

Query Match
 Best Local Similarity: 23.0%; Score 150; DB 2; Length 221;
 Matches 40; Conservative 21; Mismatches 45; Indels 12; Gaps 5;

QY 4 VAQPAVAVLASSRGISFVCEYASPGKATEVRVTVLRQADSOVTEVCATYMGNELTF 63
 D 23 VAQPAVAVLASSRGISFVCEYASPGKATEVRVTVLRQADSOVTEVCATYMGNELTF 76
 QY 64 DSI-----CTGTSSGNQVNLTIQGLRAMDTGLYICKVELMPPPYVYLGISNGTOIYVIDEPC 115
 D 77 SNSKKEFNCGIHDKDKVIFNLMMSASQTDIYCKIEAMYPYVYVNEKSNQTVIHV 134

RESULT 6
 I46197
 cell surface protein - dog (fragment)
 C:Species: Canis lupus familiaris (dog)
 C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
 C:Accession: I46197
 R:Pastori, R.L.; Milde, K.F.; Alejandro, R.

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 23, 2003, 16:43:01 ; Search time 13.5 Seconds

(Without alignments)
435.432 Million cell updates/sec

Title: US-09-865-321a-8_COPY_26_150
Sequence: 1 AMHVAQPAVVIASSRGIA SF.....GICNGTQIYIDPEPCDSD 125

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Score, No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	653	100.0	223	1	CTLA4_HUMAN
2	561	85.9	223	1	CTLA4_RABIT
3	558	85.5	223	1	CTLA4_PIG
4	458	70.1	223	1	CTLA4_MOUSE
5	150	23.0	221	1	CD28_CHICK
6	129.5	19.8	219	1	CD28_BOVIN
7	127.5	19.5	220	1	CD28_HUMAN
8	127.5	19.5	221	1	CD28_RABIT
9	121	18.5	218	1	CD28_MOUSE
10	114	17.5	218	1	CD28_RAT
11	88	13.5	111	1	LV2A_HUMAN
12	88	13.5	111	1	LV2D_HUMAN
13	85	13.0	480	1	SAHH_XANCP
14	83.5	12.8	108	1	SAHH_XANCP
15	83	12.7	111	1	KV12_RABIT
16	83	12.7	739	1	KV12_RABIT
17	81	12.4	109	1	LV2E_HUMAN
18	80.5	12.3	108	1	KV1G_HUMAN
19	80.5	12.3	108	1	KV1G_MOUSE
20	80.5	12.3	109	1	KV1G_MOUSE
21	79.5	12.2	3707	1	KV01_RAT
22	78.5	12.0	113	1	PGBM_MOUSE
23	78.5	12.0	149	1	KV5A_MOUSE
24	78	11.9	111	1	LV2H_HUMAN
25	78	11.9	480	1	SAHH_XANAC
26	78	11.9	480	1	SAHH_XANAC
27	78	11.9	480	1	SAHH_XANAC
28	78	11.9	739	1	SAHH_XANAC
29	77.5	11.9	113	1	KV1G_MOUSE
30	77	11.8	111	1	LV2C_HUMAN
31	77	11.8	129	1	LV2F_HUMAN
32	77	11.8	715	1	LOC1_LACLA
33	77	11.8	4391	1	PGBM_HUMAN

34	76.5	11.7	111	1	LV2L_HUMAN	P80422 homo sapien
35	76.5	11.7	466	1	SAHH_BRIME	O89449 bruceella me
36	76	11.6	109	1	KV3E_HUMAN	P01624 homo sapien
37	76	11.6	112	1	KV2D_MOUSE	P01629 mus musculu
38	76	11.6	114	1	KV4A_HUMAN	P01625 homo sapien
39	75.5	11.6	463	1	SAHH_CAUCR	O9ab0 caulobacter
40	75.5	11.6	485	1	SAHH_WHEAT	P32112 triticum ae
41	75	11.5	106	1	LV4B_HUMAN	P01716 homo sapien
42	75	11.5	109	1	KV4D_HUMAN	P83593 homo sapien
43	75	11.5	112	1	LV6B_HUMAN	P01722 homo sapien
44	74.5	11.4	107	1	KV6B_MOUSE	P01676 mus musculu
45	74.5	11.4	108	1	KV1V_HUMAN	P04430 homo sapien

ALIGNMENTS

RESULT 1	CTLA4_HUMAN	STANDARD	PRT: 223 AA
AC	P16410; O8WXL1; Q96P43; Q9UKN9;		
DT	01-ADG-1990 (Rel. 15, Created)		
DT	28-FEB-2003 (Rel. 41, Last sequence update)		
DT	15-SEP-2003 (Rel. 42, Last annotation update)		
DE	Cytotoxic T-lymphocyte protein 4 precursor (Cytotoxic T-lymphocyte-associated antigen 4) (CTLA-4) (CD152 antigen).		
GN	CTLA4 OR CD152.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE-21601151; PubMed-11735222;		
RA	Ling V., Wu P.W., Finnerty H.F., Agostino M.J., Graham J.R., Chen S.,		
RT	Jussif J., Fisk G.J., Miller C.P., Collins M.;		
RT	"Assembly and annotation of human chromosome 2q33 sequence containing		
RT	the CD28, CTLA4, and ICOS gene cluster: analysis by computational,		
RT	comparative, and microarray approaches.;"		
RL	Genomics 78:155-168(2001).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RX	Mu P.W., Ling V.;		
RA	"Full length sequence of hCTLA4 cDNA.;"		
RT	Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.		
RN	[3]		
RP	SEQUENCE OF 1-37 FROM N.A.		
RX	MEDLINE-9138145; PubMed-1713603;		
RA	Harper K., Balzano C., Rouvier E., Mattei M.-G., Luciani M.F.,		
RT	Golstein P.;		
RT	"CTLA-4 and CD28 activated lymphocyte molecules are closely related		
RT	in both mouse and human as to sequence, message expression, gene		
RT	structure, and chromosomal location.;"		
RL	J. Immunol. 147:1037-1044(1991).		
RN	[4]		
RP	SEQUENCE OF 38-223 FROM N.A.		
RX	TISSUE-Lymphocytes;		
RA	MEDLINE-99120925; PubMed-3220103;		
RT	Darivach P., Mattei M.-G., Golstein P., Lefranc M.-P.;		
RT	"Human Ig superfamily CTLA-4 gene: chromosomal localization and		
RT	identity of protein sequence between murine and human CTLA-4		
RT	cytoplasmic domains.;"		
RL	Eur. J. Immunol. 18:1901-1905(1988).		
RN	[5]		
RP	SEQUENCE OF 140-223 FROM N.A., AND TISSUE SPECIFICITY.		
RX	MEDLINE-99425274; PubMed-10493833;		
RA	Ling V., Wu P.W., Finnerty H.F., Sharpe A.H., Gray G.S., Collins M.;		
RT	"Complete sequence determination of the mouse and human CTLA4 gene		
RT	loci: cross-species DNA sequence similarity beyond exon borders.;"		
RL	Genomics 60:341-355(1999).		
RN	[6]		
RP	FUNCTION.		
RX	MEDLINE-91341416; PubMed-1714933;		

RA Linsley P.S., Brady W., Urnes M., Grisomatre L.S., Danle N.K.,
 RA Ledbetter J.A.,
 RT CTLA-4 is a second receptor for the B cell activation antigen B7.,
 RL J. Exp. Med. 174:561-569(1991).
 [7]
 RP STRUCTURE BY NMR OF 37-165.
 RX MEDLINE-97372889; PubMed-9228944;
 RA Metzler W.J., Bajorath J., Fenderson W., Shaw S.Y., Constantine K.L.,
 RA Naemura J., Leytze G., Peach R.J., Lavoie T.B., Mueller L.,
 RA Linsley P.S.,
 RT Solution structure of human CTLA-4 and delineation of a CD80/CD86
 RT binding site conserved in CD28.",
 RL Nat. Struct. Biol. 4:527-531(1997).
 [8]
 RP VARIANT ALA-17, AND ASSOCIATION WITH IDDM12.
 RX MEDLINE-97402209; PubMed-9259273;
 RA Marion M.P., Raffel L.J., Garchon H.-J., Jacob C.O., Serrano-Rios M.,
 RA Martinez Larrad M.T., Teng W.-P., Park Y., Zhang Z.-X.,
 RA Goldstein D.R., Tao Y.-W., Beaurain G., Bach J.-F., Huang H.-S.,
 RA Luo D.-F., Zedler A., Rottier J.I., Yang M.C.K., Modilevsky T.,
 RA MacIaren N.K., She J.-X.,
 RT "Insulin-dependent diabetes mellitus (IDDM) is associated with CTLA4
 RT polymorphisms in multiple ethnic groups.",
 RL Hum. Mol. Genet. 6:1275-1282(1997).
 [9]
 RP POLYMORPHISM, AND ASSOCIATION WITH COELIAC DISEASE.
 RX MEDLINE-99205840; PubMed-10189842;
 RA Djilali-Saah I., Schmitz J., Harfouch-Hammond E., Mougnot J.-F.,
 RA Bach J.-F., Caillaud-Zucman S.,
 RT "CTLA-4 gene polymorphism is associated with predisposition to coeliac
 RT disease.",
 RL Gut 43:187-189(1998).
 [10]
 RP VARIANT ALA-17, AND ASSOCIATION WITH TAO.
 RX MEDLINE-99402177; PubMed-10475192;
 RA Valdiva B., Imrie H., Petros P., Dickinson J., McCarthy M.I.,
 RA Kendall-Taylor P., Pearce S.H.S.,
 RT "Cytotoxic T lymphocyte antigen-4 (CTLA-4) gene polymorphism confers
 RT susceptibility to thyroid associated orbitopathy.",
 RL Lancet 354:743-744(1999).
 [11]
 RP VARIANT ALA-17, AND ASSOCIATION WITH GRD.
 RX MEDLINE-20385252; PubMed-10924276;
 RA Chistyakov D.A., Savost'yanov K.V., Turakulov R.I., Petunina N.A.,
 RA Trukhina L.V., Kudanova A.V., Balabolkin M.I., Nosikov V.V.,
 RT "Complex association analysis of Graves disease using a set of
 RT polymorphic markers.",
 RL Mol. Genet. Metab. 70:214-218(2000).
 [12]
 RP VARIANT ALA-17.
 RX MEDLINE-20395844; PubMed-10903931;
 RA Deng Z., Morse J.H., Slager S.L., Cuervo N., Moore K.J., Venetos G.,
 RA Kalachikov S., Cayanis E., Fischer S.G., Barst R.J., Hodge S.E.,
 RA Knowles J.A.,
 RT "Familial primary pulmonary hypertension (gene PPH1) is caused by
 RT mutations in the bone morphogenetic protein receptor-II gene.",
 RL Am. J. Hum. Genet. 67:737-744(2000).
 [13]
 RP FUNCTION: POSSIBLY INVOLVED IN T-CELL ACTIVATION. BINDS TO B7-1
 (CD80) AND B7-2 (CD86).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Widely expressed with highest levels in
 CC lymphoid tissues.
 CC -1- POLYMORPHISM: The variant Ala-17 is associated with an increased
 CC risk for autoimmune disorders as Graves disease (GRD), type I
 CC insulin-dependent diabetes mellitus (IDDM12), and thyroid-
 CC associated orbitopathy (TAO). The variant Thr-17 is associated
 CC with predisposition to coeliac disease, a gluten sensitive
 CC enteropathy characterized by small bowel mucosal atrophy.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
 CC -1- DATABASE: NAME-PROV: NOTE-CD guide CD152 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd152.htm".
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AF411058; AAL40932.1; -;
 CC EMBL: AF411120; AAL07473.1; -;
 CC EMBL: M74363; AAA52127.1; -;
 CC EMBL: M37245; AAA52773.1; -;
 CC EMBL: M37245; AAA52773.1; JOINED.
 CC EMBL: M37244; AAA52773.1; JOINED.
 CC EMBL: AF142144; AAF02499.1; -;
 CC PIR: S08614; S08614.
 CC PDB: 1AH1; 15-APR-98.
 CC PDB: 1H6E; 28-NOV-01.
 CC PDB: 1185; 04-APR-01.
 CC PDB: 118L; 04-APR-01.
 CC GeneW: HGNC:2505; CTLA4.
 CC MIM: 123890; -;
 CC GO: GO:0005887; C: Integral to plasma membrane; TAS.
 CC GO: GO:0006955; P: Immune response; TAS.
 CC InterPro: IPR003596; Ig_V.
 CC SMART: SM00409; IG: 1.
 CC SMART: SM00406; IG: 1.
 CC PROSITE: PS00835; IG_LIKE; FALSE_NEG.
 CC Immunoglobulin domain; T-cell; Transmembrane; Glycoprotein; Signal;
 CC 3d-structure; Polymorphism.
 CC SIGNAL 1 35
 CC CHAIN 36 223
 CC DOMAIN 36 161
 CC TRANSMEM 162 187
 CC DOMAIN 188 223
 CC DISULFID 39 140
 CC CARBOHYD 85 129
 CC DISULFID 85 103
 CC DISULFID 113 113
 CC VARIANT 17 17
 CC FT FT
 CC FT CONFLICT 147 147
 CC FT STRAND 45 47
 CC FT TURN 50 51
 CC FT STRAND 53 59
 CC FT STRAND 70 76
 CC FT STRAND 81 88
 CC FT TURN 91 92
 CC FT TURN 99 100
 CC FT STRAND 104 108
 CC FT TURN 109 110
 CC FT STRAND 111 117
 CC FT TURN 121 123
 CC FT STRAND 125 132
 CC FT TURN 137 138
 CC FT STRAND 142 143
 CC FT STRAND 147 150
 CC FT STRAND 147 150
 CC SO SEQUENCE 223 AA; 24656 MW; 6F9466FE2E139A5A CRC64;
 Query Match 100.0%; Score 653; DB 1; Length 223;
 Best Local Similarity 100.0%; Pred. No. 4; 3e-60;
 Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 AMHAPAVAVYVLIASSRGIAFVCEYASFGKATEYRVTVLROADSQVTEVCAATYMGNELT 60
 Db 37 AMHAPAVAVYVLIASSRGIAFVCEYASFGKATEYRVTVLROADSQVTEVCAATYMGNELT 96
 Oy 61 FLDDSTCTGTSSGNQVNLITGIRAMDGTGLYCKVELMTPPYLIGNCTQIYVDPDP 120
 Db 97 FLDDSTCTGTSSGNQVNLITGIRAMDGTGLYCKVELMTPPYLIGNCTQIYVDPDP 156
 Oy 121 CPDSD 125
 Db 157 CPDSD 161

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 23, 2003, 16:50:26 ; Search time 60 seconds

(without alignments)
537.610 Million cell updates/sec

Title: US-09-865-321a-8_COPY_26_150
Sequence: 1 AMHVADPAVAVLASSRGIAF.....GIGNGTQIYVIDPEPCPDS 125

Scoring table: BLOSUM62
Gap 10.0 , Gapext 0.5

Searched: 830525 segs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: SP:archaea:*
2: SP:bacteria:*
3: SP:fungi:*
4: SP:human:*
5: SP:invertebrate:*
6: SP:mammal:*
7: SP:mhc:*
8: SP:organelle:*
9: SP:phage:*
10: SP:plant:*
11: SP:rodent:*
12: SP:virus:*
13: SP:vertebrate:*
14: SP:unclassified:*
15: SP:virus:*
16: SP:bacteriap:*
17: SP:archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	648	99.2	223	6	Q9BDC4 macaca mula
2	648	99.1	223	6	Q9BDN7 papio anubi
3	647	99.1	160	4	Q8TDA6
4	601	92.0	223	6	Q9BDP1
5	597	91.4	137	4	Q9S653
6	592	90.7	115	4	Q9BZK2
7	573	87.7	223	6	Q9T02
8	573	87.7	223	6	Q9GKP2
9	571	87.4	223	11	Q9ULV3
10	569	87.1	223	6	Q9XSV7
11	566	86.7	223	6	Q9XTA1
12	559	85.6	223	6	Q9XST1
13	558	85.5	223	6	Q9N186
14	552	84.5	221	6	Q28090
15	540	82.7	221	6	Q97631
16	480	73.5	223	11	Q62859

17	425	65.1	174	11	Q9Z1A7	Q9Z1A7 rattus norv
18	252	38.6	68	11	Q99PF8	Q99PF8 cricetus
19	182	27.9	102	11	Q8CH94	Q8CH94 mus musculus
20	139	21.3	173	6	Q28289	Q28289 canis faml
21	139	21.3	221	6	Q9N08	Q9N08 canis faml
22	139	21.3	221	6	Q9GKP3	Q9GKP3 canis faml
23	136	20.8	221	11	Q9ULV4	Q9ULV4 canis faml
24	130	19.9	221	6	Q02757	Q02757 felis silve
25	129.5	19.8	219	6	Q97630	Q97630 ovis aries
26	129	19.8	221	6	Q9N214	Q9N214 felis silve
27	127.5	19.5	220	6	Q9BDM6	Q9BDM6 macaca neme
28	126.5	19.4	220	6	Q9BDN5	Q9BDN5 cercocebus
29	125.5	19.2	138	6	Q8HXR3	Q8HXR3 bos taurus
30	125	19.1	220	6	Q9BDN2	Q9BDN2 papio anubi
31	123.5	18.9	220	6	Q9BDN7	Q9BDN7 macaca mula
32	122.5	18.8	220	6	Q9BDM6	Q9BDM6 macaca mula
33	121	18.5	218	11	Q8CDB3	Q8CDB3 mus musculu
34	113	17.3	44	11	Q9Z1A8	Q9Z1A8 mus musculu
35	105	16.1	192	11	Q8CRD9	Q8CRD9 rattus norv
36	104	15.9	192	11	Q8CG11	Q8CG11 rattus norv
37	101	15.5	108	4	Q9UL79	Q9UL79 homo sapien
38	94.5	14.5	176	6	Q95JB8	Q95JB8 macaca fasc
39	94.5	14.5	180	6	Q8MJ02	Q8MJ02 macaca mula
40	91.5	14.0	177	4	Q14930	Q14930 homo sapien
41	91.5	14.0	190	4	Q14932	Q14932 homo sapien
42	91.5	14.0	201	4	Q14931	Q14931 homo sapien
43	90.5	13.9	235	11	Q91W12	Q91W12 mus musculu
44	89	13.6	151	6	Q8MJ01	Q8MJ01 macaca mula
45	88	13.5	152	4	Q95668	Q95668 homo sapien

ALIGNMENTS

Q9BDC4	PRELIMINARY;	PRT;	223 AA.
Q9BDC4	01-JUN-2001 (TREMBLrel. 17, Created)		
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)		
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)		
DE	CD152 protein precursor.		
GN	CD1A-4		
OS	Macaca mulatta (Rhesus macaque),		
OS	Macaca nemestrina (Pig-tailed macaque), and		
OS	Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;		
OC	Cercopithecoidea; Macaca.		
OX	NCBI_TaxID=9544, 9545, 9531;		
ON	[1]		
RP	SEQUENCE FROM N.A.		
RC	SPECIES=M.mulatta, M.nemestrina, and C.torquatus atys;		
RA	Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,		
RA	Weiss W.R., Ansari A.A.;		
RT	"Cloning, sequencing and homology analysis of nonhuman primate		
RT	Fas/Fas-Ligand and co-stimulatory molecules";		
RL	Immunogenetics 0:0-0(2001).		
DR	EMBL; AF344846; AAK37605.1; -		
DR	EMBL; AF344854; AAK37537.1; -		
DR	EMBL; AF344848; AAK37608.1; -		
DR	HSSP: P16410; IAH1		
DR	InterPro: IPR003596; Ig-V.		
DR	SMART: SM00406; IGV; I.		
KW	SIGNAL.		
FT	VARIANT	1	POTENTIAL.
FT	SEQUENCE	223 AA;	24683 MR; BDE4248A00398FA CRC64;
SO	SEQUENCE	223 AA;	24683 MR; BDE4248A00398FA CRC64;
Query Match	99.2%;	Score 648;	DB 6;
Best Local Similarity	98.4%;	Pred. No. 6.2e-61;	Length 223;
Matches 123;	Conservative	2;	Mismatches 0;
		Indels 0;	Gaps 0;

OY 1 AMHVAOPAVVLASSRGIASFVCEYASPGKATEVRVTVLRQADSOQVTEVCATYMMGNELT 60
 DB 37 AMHVAOPAVVLASSRGIASFVCEYASPGKATEVRVTVLRQADSOQVTEVCATYMMGNELT 96
 QY 61 FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMPPPYLLGIGNGTQIYVIDPEP 120
 DB 97 FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMPPPYLLGIGNGTQIYVIDPEP 156
 QY 121 CPDSD 125
 DB 157 CPDSD 161

RESULT 2

ID 09BDN7 PRELIMINARY; PRT; 223 AA.

AC 09BDN7;
 DT 01-JUN-2001 (TReMBLrel. 17, Created)
 DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
 DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
 DE CD152 protein precursor.
 GN CTLA-4.
 OS Papio anubis (Olive baboon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopitheciinae; Papio.
 NC NCBL_TaxID=9555;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-21383618; Pubmed-11491535;
 RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
 RA Weiss W.R., Ansari A.A.;
 RT "Cloning, sequencing, and homology analysis of nonhuman primate
 RT Fas/Fas-ligand and co-stimulatory molecules."
 RL Immunogenetics 53:315-328(2001).
 DR EMBL; AF344838; AAK37534.1; -
 DR HSSP; P16410; IAH1.
 DR InterPro; IPR003596; Ig_V.
 DR SMART; SM00406; IGV; 1.
 KW SIGNAL.
 FT SIGNAL.
 SQ SEQUENCE 223 AA; 24655 MW; EC18C279CCCC5668 CRC64;
 Query Match 99.2%; Score 648; DB 6; Length 223;
 Best Local Similarity 98.4%; Pred. No. 6,2e-61;
 Matches 123; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 OY 1 AMHVAOPAVVLASSRGIASFVCEYASPGKATEVRVTVLRQADSOQVTEVCATYMMGNELT 60
 DB 37 AMHVAOPAVVLASSRGIASFVCEYASPGKATEVRVTVLRQADSOQVTEVCATYMMGNELT 96
 QY 61 FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMPPPYLLGIGNGTQIYVIDPEP 120
 DB 97 FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMPPPYLLGIGNGTQIYVIDPEP 156
 QY 121 CPDSD 125
 DB 157 CPDSD 161

RESULT 3

ID 08TDA6 PRELIMINARY; PRT; 160 AA.

AC 08TDA6;
 DT 01-JUN-2002 (TReMBLrel. 21, Created)
 DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
 DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
 DE CTLA4 (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NC NCBL_TaxID=9606;
 RN [1]

RP SEQUENCE FROM N.A.
 RA Guo J.H., Fan M.W., Bian Z., Jia R.;
 RT "Partial sequence of CTLA4 mRNA, signal peptide and extracellular
 RT domain."
 RL Submitted (FEB-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF486806; AAL96664.1; -
 DR InterPro; IPR003596; Ig_V.
 DR SMART; SM00406; IGV; 1.
 DR NON_TER
 FT SIGNAL.
 SQ SEQUENCE 160 AA; 17470 MW; 1385B4644F63836F CRC64;

Query Match 99.1%; Score 647; DB 4; Length 160;
 Best Local Similarity 100.0%; Pred. No. 5,2e-61;

Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AMHVAOPAVVLASSRGIASFVCEYASPGKATEVRVTVLRQADSOQVTEVCATYMMGNELT 60
 DB 37 AMHVAOPAVVLASSRGIASFVCEYASPGKATEVRVTVLRQADSOQVTEVCATYMMGNELT 96
 QY 61 FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMPPPYLLGIGNGTQIYVIDPEP 120
 DB 97 FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMPPPYLLGIGNGTQIYVIDPEP 156
 QY 121 CPDSD 124
 DB 157 CPDSD 160

RESULT 4

ID 09BDP1 PRELIMINARY; PRT; 223 AA.

AC 09BDP1;
 DT 01-JUN-2001 (TReMBLrel. 17, Created)
 DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
 DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
 DE CD152 protein precursor.
 GN CTLA-4.
 OS Actus trivirgatus (Night monkey) (Douroucouli).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
 NC NCBL_TaxID=9505;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-21383618; Pubmed-11491535;
 RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
 RA Weiss W.R., Ansari A.A.;
 RT "Cloning, sequencing, and homology analysis of nonhuman primate
 RT Fas/Fas-ligand and co-stimulatory molecules."
 RL Immunogenetics 53:315-328(2001).
 DR EMBL; AF344834; AAK37530.1; -
 DR HSSP; P16410; IAH1.
 DR InterPro; IPR003599; Ig.
 DR SMART; SM00409; IGV; 1.
 KW SIGNAL.
 FT SIGNAL.
 SQ SEQUENCE 223 AA; 24813 MW; 3F702052117C1A31 CRC64;
 Query Match 92.0%; Score 601; DB 6; Length 223;
 Best Local Similarity 90.4%; Pred. No. 6,3e-56;
 Matches 113; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
 OY 1 AMHVAOPAVVLASSRGIASFVCEYASPGKATEVRVTVLRQADSOQVTEVCATYMMGNELT 60
 DB 37 AMHVAOPAVVLASSRGIASFVCEYASPGKATEVRVTVLRQADSOQVTEVCATYMMGNELT 96
 QY 61 FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMPPPYLLGIGNGTQIYVIDPEP 120
 DB 97 FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMPPPYLLGIGNGTQIYVIDPEP 156
 QY 121 CPDSD 125
 DB 157 CPDSD 161

QY 1 AMHVAOPAVYVLASSRGIAISFVCEYASPGKATEVRVTVLRQADSOVTEVCATYMMGNELT 60
 DB 37 AMHVAOPAVYVLASSRGIAISFVCEYASPGKATEVRVTVLRQADSOVTEVCATYMMGNELT 96
 QY 61 FLDDSICTGTSSGNQVNLITIGLRAMDGTGLYICKVELMPPPYLYLGINGTQIYVIDPEP 120
 DB 97 FLDDSICTGTSSGNQVNLITIGLRAMDGTGLYICKVELMPPPYLYLGINGTQIYVIDPEP 156
 QY 121 CPDSD 125
 DB 157 CPDSD 161

RESULT 2

Q9BDN7 PRELIMINARY: PRT: 223 AA.

AC 09BDN7
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE CD152 protein precursor.
 GN CTLA-4
 OS Papio anubis (Olive baboon).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
 OC Cercopitheciinae; Papio.
 CC
 CX NCBI_TaxID=9555;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-21383618; PubMed-11491535;
 RA Villinger F., Boslik P., Mayne A.E., King C.L., Genain C.P.,
 RA Weiss W.R., Ansari A.A.;
 RT "Cloning, sequencing, and homology analysis of nonhuman primate
 Fas/Fas-ligand and co-stimulatory molecules.";
 RL Immunogenetics 53:315-328(2001).
 DR EMBL; AF344838; AAK37534.1;
 DR HSSP; P16410; IAH1.
 DR InterPro; IPR003596; Iq-V.
 DR SMART; SM00406; IGV; 1.
 KW Signal.
 FT SIGNAL
 SQ SEQUENCE 223 AA; 24655 MW; EC18C279CCCC5668 CRC64;

Query Match 99.2%; Score 648; DB 6; Length 223;
 Best Local Similarity 98.4%; Pred. No. 6.2e-61;
 Matches 123; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

1 AMHVAOPAVYVLASSRGIAISFVCEYASPGKATEVRVTVLRQADSOVTEVCATYMMGNELT 60
 DB 37 AMHVAOPAVYVLASSRGIAISFVCEYASPGKATEVRVTVLRQADSOVTEVCATYMMGNELT 96
 QY 61 FLDDSICTGTSSGNQVNLITIGLRAMDGTGLYICKVELMPPPYLYLGINGTQIYVIDPEP 120
 DB 97 FLDDSICTGTSSGNQVNLITIGLRAMDGTGLYICKVELMPPPYLYLGINGTQIYVIDPEP 156

T: 160 AA.

ed)
 sequence update)
 notation update)

ta; Vertebrata; Euteleostomi;
 hml; Homidae; Homo.

RP SEQUENCE FROM N.A.
 RA Guo J.H., Fan M.W., Bian Z., Jia R.;
 RT "Partial sequence of CTLA4 mRNA, signal peptide and extracellular
 RT domain";
 RL Submitted (FE8-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF486806; AAL96664.1;
 DR InterPro; IPR003596; Iq-V.
 DR SMART; SM00406; IGV; 1.
 FT NON-TER
 SQ SEQUENCE 160 AA; 17470 MW; 1385B4644F63836F CRC64;

Query Match 99.1%; Score 647; DB 4; Length 160;
 Best Local Similarity 100.0%; Pred. No. 5.2e-61;
 Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMHVAOPAVYVLASSRGIAISFVCEYASPGKATEVRVTVLRQADSOVTEVCATYMMGNELT 60
 DB 37 AMHVAOPAVYVLASSRGIAISFVCEYASPGKATEVRVTVLRQADSOVTEVCATYMMGNELT 96
 QY 61 FLDDSICTGTSSGNQVNLITIGLRAMDGTGLYICKVELMPPPYLYLGINGTQIYVIDPEP 120
 DB 97 FLDDSICTGTSSGNQVNLITIGLRAMDGTGLYICKVELMPPPYLYLGINGTQIYVIDPEP 156
 QY 121 CPDSD 124
 DB 157 CPDSD 160

RESULT 4

Q9BDP1 PRELIMINARY: PRT: 223 AA.

AC 09BDP1
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE CD152 protein precursor.
 GN CTLA-4
 OS Aotus trivirgatus (Night monkey) (Douroucoulli).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
 CC
 CX NCBI_TaxID=9505;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-21383618; PubMed-11491535;
 RA Villinger F., Boslik P., Mayne A.E., King C.L., Genain C.P.,
 RA Weiss W.R., Ansari A.A.;
 RT "Cloning, sequencing, and homology analysis of nonhuman primate
 Fas/Fas-ligand and co-stimulatory molecules.";
 RL Immunogenetics 53:315-328(2001).
 DR EMBL; AF344834; AAK37530.1;
 DR HSSP; P16410; IAH1.
 DR InterPro; IPR003599; Iq.
 DR SMART; SM00409; IGV; 1.
 KW Signal.
 FT SIGNAL
 SQ SEQUENCE 223 AA; 24813 MW; 3F702052117C1431 CRC64;

Query Match 92.0%; Score 601; DB 6; Length 223;
 Best Local Similarity 90.4%; Pred. No. 6.3e-56;
 Matches 113; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 AMHVAOPAVYVLASSRGIAISFVCEYASPGKATEVRVTVLRQADSOVTEVCATYMMGNELT 60
 DB 37 AMHVAOPAVYVLASSRGIAISFVCEYASPGKATEVRVTVLRQADSOVTEVCATYMMGNELT 96
 QY 61 FLDDSICTGTSSGNQVNLITIGLRAMDGTGLYICKVELMPPPYLYLGINGTQIYVIDPEP 120
 DB 97 FLDDSICTGTSSGNQVNLITIGLRAMDGTGLYICKVELMPPPYLYLGINGTQIYVIDPEP 156
 QY 121 CPDSD 125
 DB 157 CPDSD 161

ersion 5.1.6
2003 Compugen Ltd.

W model

: 50.26 ; Search time 60 Seconds
(without alignments)
537.610 Million cell updates/sec

3_COPY_26_150

3SKGIAF.....GIGNCTOIVIDPECPDSD 125

0.0 ; Gapext 0.5

25 seqs, 258052604 residues

of hits satisfying chosen parameters: 830525

um DB seq length: 0
Maximum Match 0%

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_protist:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	648	99.2	223	6 O9BDC4	O9BDC4 macaca mula
2	648	99.2	223	6 O9BDC4	O9BDC4 papio anubis
3	647	99.1	160	4 O8TDA6	O8TDA6 homo sapien
4	601	92.0	223	6 O9BDP1	O9BDP1 actus trivi
5	597	91.4	137	4 O9BZK2	O9BZK2 homo sapien
6	592	90.7	115	4 O9BZK2	O9BZK2 homo sapien
7	573	87.7	223	6 O9RT02	O9RT02 canis famli
8	573	87.7	223	6 O9GKP2	O9GKP2 canis famli
9	571	87.4	223	11 O9ULV3	O9ULV3 marmota mon
10	569	87.1	223	6 O9XSY7	O9XSY7 felis silve
11	566	86.7	223	6 O9XTA1	O9XTA1 felis silve
12	559	85.6	223	6 O9XSI1	O9XSI1 canis famli
13	558	85.5	223	6 O9N186	O9N186 sus scrofa
14	552	84.5	221	6 O28090	O28090 bos taurus
15	540	82.7	221	6 O97631	O97631 ovis aries
16	480	73.5	223	11 O62859	O62859 ratius norv

17	425	65.1	174	11 O9Z1A7	O9Z1A7 ratius norv
18	252	38.6	68	11 O99PF8	O99PF8 cricetus
19	182	27.9	102	11 O8CH94	O8CH94 mus musculu
20	139	21.3	173	6 O28289	O28289 canis famli
21	139	21.3	221	6 O9N0N8	O9N0N8 canis famli
22	139	21.3	221	6 O9GKP3	O9GKP3 canis famli
23	136	20.8	221	11 O9ULV4	O9ULV4 marmota mon
24	130	19.9	221	6 O02757	O02757 felis silve
25	129.5	19.8	219	6 O97630	O97630 ovis aries
26	129	19.8	221	6 O9N214	O9N214 felis silve
27	127.5	19.5	220	6 O9BDM8	O9BDM8 macaca neme
28	126.5	19.4	220	6 O9BDM5	O9BDM5 cercocobus
29	125.5	19.2	138	6 O8HTR9	O8HTR9 bos taurus
30	125	19.1	220	6 O9BDN2	O9BDN2 callithrix
31	123.5	18.9	220	6 O9BDN8	O9BDN8 papio anubis
32	122.5	18.8	220	6 O9BDM6	O9BDM6 macaca mula
33	121	18.5	218	11 O8CDB3	O8CDB3 mus musculu
34	113	17.3	44	11 O9Z1A8	O9Z1A8 mus musculu
35	105	16.1	192	11 O8CFD9	O8CFD9 ratius norv
36	104	15.9	192	11 O8CG11	O8CG11 ratius norv
37	101	15.5	108	4 O9UL79	O9UL79 homo sapien
38	94.5	14.5	176	6 O95JH8	O95JH8 macaca faec
39	94.5	14.5	180	6 O8MJ02	O8MJ02 macaca mula
40	91.5	14.0	177	4 O14930	O14930 homo sapien
41	91.5	14.0	190	4 O14932	O14932 homo sapien
42	91.5	14.0	201	4 O14931	O14931 homo sapien
43	90.5	13.9	235	11 O91W12	O91W12 mus musculu
44	89	13.6	151	6 O8MJ01	O8MJ01 macaca mula
45	88	13.5	152	4 O95668	O95668 homo sapien

ALIGNMENTS

RESULT 1					
ID	O9BDC4	PRELIMINARY:	PRT:	223 AA.	
AC	O9BDC4:				
DT	01-JUN-2001 (TREMBLrel. 17, Created)				
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)				
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)				
DE	CD152 protein precursor.				
GN	CTLA-4.				
OS	Macaca mulatta (Rhesus macaque),				
OS	Macaca nemestrina (Pig-tailed macaque), and				
OS	Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;				
OC	Cercopithecinae; Macaca.				
OX	NCBI_TaxID=9544, 9545, 9531;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
KC	SPECIES=M.mulatta, M.nemestrina, and C.torquatus atys;				
RA	Villinger F., Bostik P., Wayne A.E., King C.L., Genain C.P.,				
RA	Weiss W.R., Ansari A.A.;				
RT	"Cloning, sequencing and homology analysis of nonhuman primate				
RT	Fas/Fas-ligand and co-stimulatory molecules."				
RL	Immunogenetics 0:0-0(2001);				
RL	EMBL; AF344846; AAK37605.1;				
DR	EMBL; AF344846; AAK37537.1;				
DR	EMBL; AF344848; AAK37608.1;				
DR	HSSP; P16410; 1AH1.				
DR	Interpro: IPR003596; IG-V.				
DR	SMART: SM00406; IGV; 1.				
KW	Signal.				
FT	SIGNAL	1	37	POTENTIAL.	
FT	VARIANT	223	223	N->D.	
SO	SEQUENCE	223 AA;	24683 MM;	BDE42248A0398FA CRC64;	
Query Match		99.2%	Score 648;	DB 6;	Length 223;
Best Local Similarity		98.4%	Pred. No. 6.2e-61;		
Matches	123;	Conservative	2;	Mismatches	0;
				Indels	0;
				Gaps	0;

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 23, 2003, 16:57:06 ; Search time 36 Seconds

(without alignments)
458,200 Million cell updates/sec

Title: US-09-865-321a-8_copy_26_150

Perfect score: 653
Sequence: 1 AMHVAQPAVVLASSRGIAASF.....GICNGTQIYVIDPECPDSD 125

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 497079 seqs, 131961718 residues

Total number of hits satisfying chosen parameters: 497079

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubppaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubppaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubppaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubppaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubppaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubppaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubppaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubppaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubppaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubppaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubppaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubppaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubppaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	653	100.0	151	US-10-207-655-309	Sequence 309, App
2	653	100.0	212	US-09-898-195A-17	Sequence 17, App1
3	653	100.0	212	US-10-057-288-12	Sequence 12, App1
4	653	100.0	212	US-10-155-514-2	Sequence 2, App1
5	653	100.0	374	US-10-027-075-26	Sequence 26, App1
6	653	100.0	374	US-10-027-075-24	Sequence 26, App1
7	653	100.0	377	US-10-027-075-24	Sequence 26, App1
8	653	100.0	382	US-10-207-655-307	Sequence 307, App
9	653	100.0	382	US-10-207-655-316	Sequence 316, App
10	653	100.0	383	US-09-865-321-8	Sequence 8, App1
11	653	100.0	383	US-09-898-195A-19	Sequence 19, App1
12	653	100.0	383	US-10-057-288-14	Sequence 14, App1
13	653	100.0	383	US-10-155-514-4	Sequence 4, App1
14	653	100.0	383	US-10-155-514-16	Sequence 16, App1
15	653	100.0	399	US-10-207-655-320	Sequence 320, App

16	653	100.0	403	15	US-10-207-655-318	Sequence 318, App
17	648	99.2	223	11	US-09-835-297-2	Sequence 2, App1
18	648	99.2	223	15	US-10-211-207-3	Sequence 3, App1
19	647	99.1	168	10	US-09-845-899A-7	Sequence 7, App1
20	647	99.1	223	10	US-09-989-545-21	Sequence 21, App1
21	647	99.1	223	15	US-10-225-519-8	Sequence 8, App1
22	647	99.1	223	15	US-10-207-655-101	Sequence 101, App
23	646	98.9	383	10	US-09-865-321-6	Sequence 6, App1
24	646	98.9	383	11	US-09-898-195A-7	Sequence 7, App1
25	646	98.9	383	15	US-10-057-288-2	Sequence 2, App1
26	646	98.9	383	15	US-10-155-519-4	Sequence 4, App1
27	643	98.5	260	15	US-10-225-519-8	Sequence 8, App1
28	642	98.3	383	11	US-09-898-195A-13	Sequence 13, App1
29	642	98.3	383	15	US-10-057-288-8	Sequence 8, App1
30	642	98.3	383	15	US-10-155-514-12	Sequence 12, App1
31	641	98.2	124	15	US-10-207-655-314	Sequence 314, App
32	641	98.2	383	11	US-09-898-195A-11	Sequence 11, App1
33	641	98.2	383	15	US-10-057-288-6	Sequence 6, App1
34	641	98.2	383	15	US-10-155-514-10	Sequence 10, App1
35	640	98.0	187	11	US-09-014-761-1	Sequence 1, App1
36	640	98.0	223	14	US-10-107-828-26	Sequence 26, App1
37	640	98.0	223	14	US-10-107-807-26	Sequence 26, App1
38	640	98.0	223	14	US-10-107-868-26	Sequence 26, App1
39	640	98.0	223	15	US-10-301-056-26	Sequence 26, App1
40	640	98.0	383	10	US-09-865-321-4	Sequence 4, App1
41	640	98.0	383	11	US-09-898-195A-9	Sequence 9, App1
42	640	98.0	383	15	US-10-057-288-4	Sequence 4, App1
43	640	98.0	383	15	US-10-155-514-6	Sequence 6, App1
44	639	97.9	383	11	US-09-898-195A-15	Sequence 15, App1
45	639	97.9	383	15	US-10-057-288-10	Sequence 10, App1

ALIGNMENTS

RESULT 1
US-10-207-655-309
Sequence 309, Application US/10207655
Publication No. US20030118592A1
GENERAL INFORMATION:
APPLICANT: Ledbetter, Jeffrey A.
TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
FILE REFERENCE: 390069.401C1
CURRENT APPLICATION NUMBER: US/10/207,655
CURRENT FILING DATE: 2002-07-25
NUMBER OF SEQ ID NOS: 426
SOFTWARE: PatentIn version 3.0
SEQ ID NO 309
LENGTH: 151
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: fusion polypeptide
US-10-207-655-309

Query Match	100.0%	Score 653	DB 15	Length 151
Best Local Similarity	100.0%	Pred. No. 1.4e-62		
Matches 125	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	AMHVAQPAVVLASSRGIAFVCEYASPGKATEVAVTLROADSQVTEVCATYMGNELT	60	
DB	26	AMHVAQPAVVLASSRGIAFVCEYASPGKATEVAVTLROADSQVTEVCATYMGNELT	85	
QY	61	FLDSDICTGSSGNQVNLITGGLRAMDTGLYICKVEIMPPPYLGLGNGTQIYVIDPEP	120	
DB	86	FLDSDICTGSSGNQVNLITGGLRAMDTGLYICKVEIMPPPYLGLGNGTQIYVIDPEP	145	
QY	121	CPDSD 125		
DB	146	CPDSD 150		

```
RESULT 2
US-09-898-195A-17
; Sequence 17, Application US/09898195A
; Publication No. US20030083246A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Robert
; APPLICANT: Carr, Suzanne
; APPLICANT: Hagerly, David
; APPLICANT: Peach, Robert J
; APPLICANT: Becker, Jean-Claude
; TITLE OF INVENTION: METHODS FOR TREATING RHEUMATIC DISEASES USING A SOLUBLE
; FILE REFERENCE: D0030NF/30436.55USU1
; CURRENT APPLICATION NUMBER: US/09/898,195A
; PRIOR FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: 60/215,913
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-898-195A-17

Query Match          100.0%; Score 653; DB 11; Length 212;
Best Local Similarity 100.0%; Pred. No. 2,1e-62;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMHVAQPAVVLASSRGISAFVCEYASPGKATEVRVTVLRQADSOVTEVCATYMMGNELT 60
    |||||||
DB 26 AMHVAQPAVVLASSRGISAFVCEYASPGKATEVRVTVLRQADSOVTEVCATYMMGNELT 85
    |||||||

QY 61 FLDDISCTGTSSGNOVNLTIGLRAMDGLYICKVELMPPPYLYGIGNGTQIYVIDEP 120
    |||||||
DB 86 FLDDISCTGTSSGNOVNLTIGLRAMDGLYICKVELMPPPYLYGIGNGTQIYVIDEP 145
    |||||||

QY 121 CPDSD 125
    |||||
DB 146 CPDSD 150

RESULT 3
US-10-057-288-12
; Sequence 12, Application US/10057288
; Publication No. US20030007968A1
; GENERAL INFORMATION:
; APPLICANT: Larsen, Christian P.
; APPLICANT: Pearson, Thomas C.
; APPLICANT: Waller, Edmund K.
; APPLICANT: Adams, Andrew B.
; TITLE OF INVENTION: METHODS OF INDUCING ORGAN TRANSPLANT TOLERANCE AND
; FILE REFERENCE: D0136NP/30436.580SU1
; CURRENT APPLICATION NUMBER: US/10/057,288
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: 60/264,528
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/303,142
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-057-288-12

Query Match          100.0%; Score 653; DB 15; Length 212;
Best Local Similarity 100.0%; Pred. No. 2,1e-62;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMHVAQPAVVLASSRGISAFVCEYASPGKATEVRVTVLRQADSOVTEVCATYMMGNELT 60
    |||||||
DB 26 AMHVAQPAVVLASSRGISAFVCEYASPGKATEVRVTVLRQADSOVTEVCATYMMGNELT 85
    |||||||

QY 61 FLDDISCTGTSSGNOVNLTIGLRAMDGLYICKVELMPPPYLYGIGNGTQIYVIDEP 120
    |||||||
DB 86 FLDDISCTGTSSGNOVNLTIGLRAMDGLYICKVELMPPPYLYGIGNGTQIYVIDEP 145
    |||||||

QY 121 CPDSD 125
    |||||
DB 146 CPDSD 150
```

```
DB 26 AMHVAQPAVVLASSRGISAFVCEYASPGKATEVRVTVLRQADSOVTEVCATYMMGNELT 85
    |||||||
QY 61 FLDDISCTGTSSGNOVNLTIGLRAMDGLYICKVELMPPPYLYGIGNGTQIYVIDEP 120
    |||||||
DB 86 FLDDISCTGTSSGNOVNLTIGLRAMDGLYICKVELMPPPYLYGIGNGTQIYVIDEP 145
    |||||||

QY 121 CPDSD 125
    |||||
DB 146 CPDSD 150

RESULT 4
US-10-155-514-2
; Sequence 2, Application US/10155514
; Publication No. US20030022836A1
; GENERAL INFORMATION:
; APPLICANT: Larsen, Christian P.
; APPLICANT: Pearson, Thomas C.
; APPLICANT: Adams, Andrew B.
; TITLE OF INVENTION: METHODS FOR PROTECTING ALLOGENEIC ISLET TRANSPLANT USING SOLUB
; FILE REFERENCE: D0173NP / 30436.620SU1
; CURRENT APPLICATION NUMBER: US/10/155,514
; PRIOR FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: 60/293,402
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-155-514-2

Query Match          100.0%; Score 653; DB 15; Length 212;
Best Local Similarity 100.0%; Pred. No. 2,1e-62;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMHVAQPAVVLASSRGISAFVCEYASPGKATEVRVTVLRQADSOVTEVCATYMMGNELT 60
    |||||||
DB 26 AMHVAQPAVVLASSRGISAFVCEYASPGKATEVRVTVLRQADSOVTEVCATYMMGNELT 85
    |||||||

QY 61 FLDDISCTGTSSGNOVNLTIGLRAMDGLYICKVELMPPPYLYGIGNGTQIYVIDEP 120
    |||||||
DB 86 FLDDISCTGTSSGNOVNLTIGLRAMDGLYICKVELMPPPYLYGIGNGTQIYVIDEP 145
    |||||||

QY 121 CPDSD 125
    |||||
DB 146 CPDSD 150

RESULT 5
US-10-027-075-26
; Sequence 26, Application US/10027075
; Publication No. US20020114814A1
; GENERAL INFORMATION:
; APPLICANT: Gray, Gary S. et al.
; TITLE OF INVENTION: CTLA4-Immunoglobulin Fusion Proteins
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESS: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
```

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 23, 2003, 16:52:21 ; Search time 20.5 Seconds
(without alignments)
257.993 Million cell updates/sec

Title: US-09-865-321a-8_COPY_26_150

Perfect score: 653
Sequence: 1 AMHYAOPAVYVLAASSRGIAASF.....GIGNGTQIYVIDPECPDSD 125

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310658 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA: *
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep: *
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep: *
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/PCITUS.COMB.pep: *
6: /cgn2_6/ptodata/1/1aa/Backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	653	100.0	187	1 US-08-067-684-14	Sequence 14, Appl
2	653	100.0	187	1 US-08-008-898-14	Sequence 14, Appl
3	653	100.0	187	2 US-08-459-818-14	Sequence 14, Appl
4	653	100.0	187	2 US-08-889-666-14	Sequence 14, Appl
5	653	100.0	187	2 US-08-455-078-14	Sequence 14, Appl
6	653	100.0	187	2 US-08-725-776-14	Sequence 14, Appl
7	653	100.0	187	2 US-08-488-062-14	Sequence 14, Appl
8	653	100.0	187	3 US-08-228-208A-14	Sequence 14, Appl
9	653	100.0	223	4 US-08-228-208A-17	Sequence 17, Appl
10	653	100.0	374	4 US-08-227-595-26	Sequence 26, Appl
11	653	100.0	374	4 US-08-227-595-28	Sequence 28, Appl
12	653	100.0	374	4 US-08-227-595-24	Sequence 24, Appl
13	650	99.5	187	5 PCT-US95-06726-36	Sequence 36, Appl
14	644	98.6	124	3 US-08-630-172-4	Sequence 4, Appl
15	644	98.6	124	3 US-09-375-419-4	Sequence 4, Appl
16	644	98.6	357	3 US-08-630-172-20	Sequence 20, Appl
17	644	98.6	357	3 US-09-375-419-20	Sequence 20, Appl
18	630.5	96.6	253	2 US-08-459-818-20	Sequence 20, Appl
19	630.5	96.6	253	2 US-08-889-666-20	Sequence 20, Appl
20	630.5	96.6	253	2 US-08-465-078-20	Sequence 20, Appl
21	630.5	96.6	253	2 US-08-725-776-20	Sequence 20, Appl
22	630.5	96.6	253	2 US-08-488-062-20	Sequence 20, Appl
23	630.5	96.6	502	2 US-08-459-818-19	Sequence 19, Appl
24	630.5	96.6	502	2 US-08-889-666-19	Sequence 19, Appl
25	630.5	96.6	502	2 US-08-465-078-19	Sequence 19, Appl
26	630.5	96.6	502	2 US-08-725-776-19	Sequence 19, Appl
27	630.5	96.6	502	2 US-08-488-062-19	Sequence 19, Appl

28	613	93.9	234	1 US-08-505-058-1	Sequence 1, Appl
29	613	93.9	234	2 US-08-459-818-21	Sequence 21, Appl
30	613	93.9	234	2 US-08-889-666-21	Sequence 21, Appl
31	613	93.9	234	2 US-08-465-078-21	Sequence 21, Appl
32	613	93.9	234	2 US-08-725-776-21	Sequence 21, Appl
33	613	93.9	234	2 US-08-488-062-21	Sequence 21, Appl
34	597	91.4	137	3 US-08-804-180C-2	Sequence 30, Appl
35	583	89.3	238	4 US-09-227-595-30	Sequence 32, Appl
36	583	89.3	238	4 US-09-227-595-32	Sequence 32, Appl
37	563	86.2	109	4 US-09-460-384-34	Sequence 34, Appl
38	547	83.8	223	3 US-09-303-040-10	Sequence 18, Appl
39	439	67.2	223	3 US-08-228-208A-18	Sequence 10, Appl
40	425	65.1	174	3 US-08-804-180C-4	Sequence 4, Appl
41	408	62.5	234	1 US-08-505-058-2	Sequence 2, Appl
42	408	62.5	234	2 US-08-458-818-22	Sequence 22, Appl
43	408	62.5	234	2 US-08-889-666-22	Sequence 22, Appl
44	408	62.5	234	2 US-08-465-078-22	Sequence 22, Appl
45	408	62.5	234	2 US-08-725-776-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1
US-08-067-684-14
Sequence 14, Application US/08067684
Patent No. 5434131
GENERAL INFORMATION:
APPLICANT: Linsley, Peter S.
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Damle, Nitin K.
APPLICANT: Brady, William
TITLE OF INVENTION: CTLA4 RECEPTOR AND METHODS FOR ITS USE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, Suite 900
CITY: Pasadena
STATE: California
COUNTRY: U.S.A.
ZIP: 91101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/067,684
FILING DATE: 26-MAY-1993
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B.
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 7848-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310/479-8340
TELEFAX: 310/312-9900
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 187 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-067-684-14
Query Match 100.0%; Score 653; DB 1; Length 187;
Best Local Similarity 100.0%; Pred. No. 2.4e-63;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 AMHYAOPAVYVLAASSRGIASFVCEYASPGKATEYRVTVLRQADSQVTEVCATYMGNEILT 60
|||||

Db 1 AMHVAOPAVVLASSRGIAFVCEYASPGKATEVRVTVLRQADSOVTEVCATYMMGNELT 60
QY 61 FLDDSGTGTSSGNQVNLTIQGLRAMDGLYICKVELMPPPYIIGNGTOIYVIDEP 120
Db 61 FLDDSGTGTSSGNQVNLTIQGLRAMDGLYICKVELMPPPYIIGNGTOIYVIDEP 120
QY 121 CPDSD 125
Db 121 CPDSD 125

RESULT 2

US-08-008-898-14
Sequence 14, Application US/08008898
Patent No. 5770197
GENERAL INFORMATION:
APPLICANT: Linsley, Peter S
APPLICANT: Ledbetter, Jeffrey A
APPLICANT: Dame, Milton K
APPLICANT: Brady, William
TITLE OF INVENTION: CTLA4 RECEPTOR AND METHODS FOR ITS USE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Max
STREET: 201 South Lake Avenue, Suite 800
CITY: Pasadena
STATE: California
COUNTRY: United States
ZIP: 91101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/008.898
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/723.617
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mandel, Saralynn
REGISTRATION NUMBER: 31,853
REFERENCE/DOCKET NUMBER: 7848
TELECOMMUNICATION INFORMATION:
TELEPHONE: (818) 796-4000
TELEFAX: (818) 795-6321
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 187 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-008-898-14

Query Match 100.0%; Score 653; DB 1; Length 187;
Best Local Similarity 100.0%; Pred. No. 2.4e-63;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMHVAOPAVVLASSRGIAFVCEYASPGKATEVRVTVLRQADSOVTEVCATYMMGNELT 60
Db 1 AMHVAOPAVVLASSRGIAFVCEYASPGKATEVRVTVLRQADSOVTEVCATYMMGNELT 60
QY 61 FLDDSGTGTSSGNQVNLTIQGLRAMDGLYICKVELMPPPYIIGNGTOIYVIDEP 120
Db 61 FLDDSGTGTSSGNQVNLTIQGLRAMDGLYICKVELMPPPYIIGNGTOIYVIDEP 120
QY 121 CPDSD 125
Db 121 CPDSD 125

RESULT 3

US-08-459-818-14
Sequence 14, Application US/08459818
Patent No. 5851795
GENERAL INFORMATION:
APPLICANT: Linsley, Peter S.
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Dame, Milton K.
APPLICANT: Brady, William
TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 11150 Santa Monica Blvd., Suite 400
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FastSeq 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459.818
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B.
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 30436.35US02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 187 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-818-14

Query Match 100.0%; Score 653; DB 2; Length 187;
Best Local Similarity 100.0%; Pred. No. 2.4e-63;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMHVAOPAVVLASSRGIAFVCEYASPGKATEVRVTVLRQADSOVTEVCATYMMGNELT 60
Db 1 AMHVAOPAVVLASSRGIAFVCEYASPGKATEVRVTVLRQADSOVTEVCATYMMGNELT 60
QY 61 FLDDSGTGTSSGNQVNLTIQGLRAMDGLYICKVELMPPPYIIGNGTOIYVIDEP 120
Db 61 FLDDSGTGTSSGNQVNLTIQGLRAMDGLYICKVELMPPPYIIGNGTOIYVIDEP 120
QY 121 CPDSD 125
Db 121 CPDSD 125

RESULT 4

US-08-889-666-14
Sequence 14, Application US/08889666
Patent No. 5885579
GENERAL INFORMATION:
APPLICANT: Linsley, Peter S.
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Dame, Milton K.
APPLICANT: Brady, William
APPLICANT: Kienert, Peter A.
TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould